

**SEQUENCE LISTING**

<110> University of Florida Research Foundation, Inc.  
Hannah, L. Curtis  
Lyerly Linebarger, Carla R.

<120> Heat Stable Variants of Adenosine Diphosphate Glucose Pyrophosphorylase

6130> UF.371XC1

<140> 10/569,000  
<141> 2006-10-10

<150> PCT/US2004/026965

<151> 2004-08-18

<150> 60/496,188

<151> 2003-08-18

<160> 42

<170> PatentIn version 3.2

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35 40 45	

Ile Leu Gly Gly Ala Gly Thr Arg Leu Tyr Pro Leu Thr Lys Lys	
50 55 60	

Arg Ala Lys Pro Ala Val Pro Leu Gly Ala Asn Tyr Arg Leu Ile Asp	
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Ile Pro Val Ser Asn Cys Leu Asn Ser Asn Ile Ser Lys Ile Tyr Val	
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Tyr Gly Ser Asn Ile Gly Gly Tyr Lys Asn Glu Gly Phe Val Glu Val	
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Ala Asp Ala Val Arg Gln Tyr Leu Trp Leu Phe Glu Glu His Asn Val

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Lys Ile Asp Glu Glu Gly Arg Ile Ile Glu Phe Ala Glu Lys Pro Lys			
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Asp Asp Val Arg Ala Lys Glu Met Pro Tyr Ile Ala Ser Met Gly Ile			
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Tyr Val Phe Ser Lys Asp Val Met Leu Gln Leu Leu Arg Glu Gln Phe			
260	265	270	
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Ile Gly Lys Arg Val Gln Ala Tyr Leu Tyr Asp Gly Tyr Trp Glu Asp			
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Ile Gly Thr Ile Ala Ala Phe Tyr Asn Ala Asn Leu Gly Ile Thr Lys			
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Lys Pro Ile Pro Asp Phe Ser Phe Tyr Asp Arg Phe Ala Pro Ile Tyr			
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Thr Gln Pro Arg His Leu Pro Pro Ser Lys Val Leu Asp Ala Asp Val			
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Thr Asp Ser Val Ile Gly Glu Gly Cys Val Ile Lys Asn Cys Lys Ile			
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Asn His Ser Val Val Gly Leu Arg Ser Cys Ile Ser Glu Gly Ala Ile			
370	375	380	
Ile Glu Asp Ser Leu Leu Met Gly Ala Asp Tyr Tyr Glu Thr Glu Ala			
385	390	395	400
Asp Lys Lys Leu Leu Ala Glu Lys Gly Ile Pro Ile Gly Ile Gly			
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Lys Asn Ser Cys Ile Arg Arg Ala Ile Ile Asp Lys Asn Ala Arg Ile			
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attcctgtca gcaattgtct caacagcaac atatccaaga tctatgtgt aacgcattt 300  
aactctgttt ccctcaacccg tcacccctca agagcctacg ggagcaacat tggagggtac 360  
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35 40 45	
Ile Leu Gly Gly Ala Gly Thr Arg Leu Tyr Pro Leu Thr Lys Lys	
50 55 60	
Arg Ala Lys Pro Ala Val Pro Leu Gly Ala Asn Tyr Arg Leu Ile Asp	
65 70 75 80	
Ile Pro Val Ser Asn Cys Leu Asn Ser Asn Ile Ser Lys Ile Tyr Val	
85 90 95	
Leu Thr Gln Phe Asn Ser Ala Ser Leu Asn Arg His Leu Ser Arg Ala	
100 105 110	
Tyr Gly Ser Asn Ile Gly Gly Tyr Lys Asn Glu Gly Phe Val Glu Val	
115 120 125	
Leu Ala Ala Gln Gln Ser Pro Asp Asn Pro Asn Trp Phe Gln Gly Thr	
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Ala Asp Ala Val Arg Gln Tyr Leu Trp Leu Phe Glu Glu His Asn Val	
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165 170 175	
Glu Lys Phe Ile Gln Ala His Arg Glu Thr Asn Ala Asp Ile Thr Val	
180 185 190	
Ala Ala Leu Pro Met Asp Glu Lys Arg Ala Thr Ala Phe Gly Leu Met	
195 200 205	
Lys Ile Asp Glu Glu Gly Arg Ile Ile Glu Phe Ala Glu Lys Pro Lys	
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Gly Glu Gln Leu Lys Ala Met Met Val Asp Thr Thr Ile Leu Gly Leu	
225 230 235 240	

Asp Asp Val Arg Ala Lys Glu Met Pro Tyr Ile Ala Ser Met Gly Ile  
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Tyr Val Phe Ser Lys Asp Val Met Leu Gln Leu Leu Arg Glu Gln Phe  
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Pro Glu Ala Asn Asp Phe Gly Ser Glu Val Ile Pro Gly Ala Thr Ser  
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Ile Gly Lys Arg Val Gln Ala Tyr Leu Tyr Asp Gly Tyr Trp Glu Asp  
290 295 300

Ile Gly Thr Ile Ala Ala Phe Tyr Asn Ala Asn Leu Gly Ile Thr Lys  
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Lys Pro Ile Pro Asp Phe Ser Phe Tyr Asp Arg Phe Ala Pro Ile Tyr  
325 330 335

Thr Gln Pro Arg His Leu Pro Pro Ser Lys Val Leu Asp Ala Asp Val  
340 345 350

Thr Asp Ser Val Ile Gly Glu Gly Cys Val Ile Lys Asn Cys Lys Ile  
355 360 365

Asn His Ser Val Val Gly Leu Arg Ser Cys Ile Ser Glu Gly Ala Ile  
370 375 380

Ile Glu Asp Ser Leu Leu Met Gly Ala Asp Tyr Tyr Glu Thr Glu Ala  
385 390 395 400

Asp Lys Lys Leu Leu Ala Glu Lys Gly Ile Pro Ile Gly Ile Gly  
405 410 415

Lys Asn Ser Cys Ile Arg Arg Ala Ile Ile Asp Lys Asn Ala Arg Ile  
420 425 430

Gly Asp Asn Val Lys Ile Leu Asn Ala Asp Asn Val Gln Glu Ala Ala  
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 35 40 45

Ile Ile Leu Gly Gly Ala Gly Thr Arg Leu Tyr Pro Leu Thr Lys  
 50 55 60

Lys Arg Ala Lys Pro Ala Val Pro Leu Gly Ala Asn Tyr Arg Leu Ile  
 65 70 75 80

Asp Ile Pro Val Ser Asn Cys Leu Asn Ser Asn Ile Ser Lys Ile Tyr  
 85 90 95

Val Leu Thr Gln Phe Asn Ser Ala Ser Leu Asn Arg His Leu Ser Arg  
 100 105 110

Ala Tyr Gly Ser Asn Ile Gly Gly Tyr Lys Asn Glu Gly Phe Val Glu  
 115 120 125

Val Leu Ala Ala Gln Gln Ser Pro Asp Asn Pro Asn Trp Phe Gln Gly  
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Thr Ala Asp Ala Val Arg Gln Tyr Leu Trp Leu Phe Glu Glu His Asn  
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Val Met Glu Phe Leu Ile Leu Ala Gly Asp His Leu Tyr Arg Met Asp  
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Tyr Glu Lys Phe Ile Gln Ala His Arg Glu Thr Asn Ala Asp Ile Thr  
 180 185 190

Val Ala Ala Leu Pro Met Asp Glu Lys Arg Ala Thr Ala Phe Gly Leu  
 195 200 205

Met Lys Ile Asp Glu Glu Gly Arg Ile Ile Glu Phe Ala Glu Lys Pro  
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Lys Gly Glu Gln Leu Lys Ala Met Met Val Asp Thr Thr Ile Leu Gly  
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Leu Asp Asp Val Arg Ala Lys Glu Met Pro Tyr Ile Ala Ser Met Gly  
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Ile Tyr Val Phe Ser Lys Asp Val Met Leu Gln Leu Leu Arg Glu Gln  
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Phe Pro Glu Ala Asn Asp Phe Gly Ser Glu Val Ile Pro Gly Ala Thr  
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Ser Ile Gly Lys Arg Val Gln Ala Tyr Leu Tyr Asp Gly Tyr Trp Glu  
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Asp Ile Gly Thr Ile Ala Ala Phe Tyr Asn Ala Asn Leu Gly Ile Thr  
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Lys Lys Pro Ile Pro Asp Phe Ser Phe Tyr Asp Arg Phe Ala Pro Ile

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Tyr Thr Gln Pro Arg His Leu Pro Pro Ser Lys Val Leu Asp Ala Asp			
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Val Thr Asp Ser Val Ile Gly Glu Gly Cys Val Ile Lys Asn Cys Lys			
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Ile Asn His Ser Val Val Gly Leu Arg Ser Cys Ile Ser Glu Gly Ala			
370	375	380	
Ile Ile Glu Asp Ser Leu Leu Met Gly Ala Asp Tyr Tyr Glu Thr Glu			
385	390	395	400
Ala Asp Lys Lys Leu Leu Ala Glu Lys Gly Gly Ile Pro Ile Gly Ile			
405	410	415	
Gly Lys Asn Ser Cys Ile Arg Arg Ala Ile Ile Asp Lys Asn Ala Arg			
420	425	430	
Ile Gly Asp Asn Val Lys Ile Leu Asn Ala Asp Asn Val Gln Glu Ala			
435	440	445	
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Asp	Ser	Gln	Thr	Cys	Leu	Asn	Pro	Gln	Ala	His	Asp	Ser	Val	Leu	Gly
															45

Ile	Ile	Leu	Gly	Gly	Ala	Gly	Thr	Arg	Leu	Tyr	Pro	Leu	Thr	Lys	
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Lys	Arg	Ala	Lys	Pro	Ala	Val	Pro	Leu	Gly	Ala	Asn	Tyr	Arg	Leu	Ile
															65
															80

Asp	Ile	Pro	Val	Ser	Asn	Cys	Leu	Asn	Ser	Asn	Ile	Ser	Lys	Ile	Tyr
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Val	Leu	Thr	Gln	Phe	Asn	Ser	Ala	Ser	Leu	Asn	Arg	His	Leu	Ser	Arg
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															105

Ala	Tyr	Gly	Ser	Asn	Ile	Gly	Gly	Tyr	Lys	Asn	Glu	Gly	Phe	Val	Glu
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Val Met Glu Phe Leu Ile Leu Ala Gly Asp His Leu Tyr Arg Met Asp		
165	170	175
Tyr Glu Lys Phe Ile Gln Ala His Arg Glu Thr Asn Ala Asp Ile Thr		
180	185	190
Val Ala Ala Leu Pro Met Asp Glu Lys Arg Ala Thr Ala Phe Gly Leu		
195	200	205
Met Lys Ile Asp Glu Glu Gly Arg Ile Ile Glu Phe Ala Glu Lys Pro		
210	215	220
Lys Gly Glu Gln Leu Lys Ala Met Met Val Asp Thr Thr Ile Leu Gly		
225	230	235
Leu Asp Asp Val Arg Ala Lys Glu Met Pro Tyr Ile Ala Ser Met Gly		
245	250	255
Ile Tyr Val Phe Ser Lys Asp Val Met Leu Gln Leu Leu Arg Glu Gln		
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Phe Pro Glu Ala Asn Asp Phe Gly Ser Glu Val Ile Pro Gly Ala Thr		
275	280	285
Ser Ile Gly Lys Arg Val Gln Ala Tyr Leu Tyr Asp Gly Tyr Trp Glu		
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Asp Ile Gly Thr Ile Ala Ala Phe Tyr Asn Ala Asn Leu Gly Ile Thr		
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Lys Lys Pro Ile Pro Asp Phe Ser Phe Tyr Asp Arg Phe Ala Pro Ile		
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Tyr Thr Gln Pro Arg His Leu Pro Pro Ser Lys Val Leu Asp Ala Asp		
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Val Thr Asp Ser Val Ile Gly Glu Gly Cys Val Ile Lys Asn Cys Lys		
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Ile Asn His Ser Val Val Gly Leu Arg Ser Cys Ile Ser Glu Gly Ala		
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Ile Ile Glu Asp Ser Leu Leu Met Gly Ala Asp Tyr Tyr Glu Thr Glu		
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Ala Asp Lys Lys Leu Leu Ala Glu Lys Gly Gly Ile Pro Ile Gly Ile		
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Gly Lys Asn Ser Cys Ile Arg Arg Ala Ile Ile Asp Lys Asn Ala Arg		



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Ile Ile Leu Gly Gly Ala Gly Thr Arg Leu Tyr Pro Leu Thr Lys	
50 55 60	

Lys Arg Ala Lys Pro Ala Val Pro Leu Gly Ala Asn Tyr Arg Leu Ile	
65 70 75 80	

Asp Ile Pro Val Ser Asn Cys Leu Asn Ser Asn Ile Ser Lys Ile Tyr	
85 90 95	

Val Leu Thr Gln Phe Asn Ser Ala Ser Leu Asn Arg His Leu Ser Arg	
100 105 110	

Ala Tyr Gly Ser Asn Ile Gly Gly Tyr Lys Asn Glu Gly Phe Val Glu	
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Val Leu Ala Ala Gln Gln Ser Pro Asp Asn Pro Asn Trp Phe Gln Gly	
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Thr Ala Asp Ala Val Arg Gln Tyr Leu Trp Leu Phe Glu Glu His Asn	
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Met Lys Ile Asp Glu Glu Gly Arg Ile Ile Glu Phe Ala Glu Lys Pro

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 <223> k = g or t.

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 ggaggagat atg cag ttt gca ctt gca ttg gac acg aac tca ggt cct cac 51  
 Met Gln Phe Ala Leu Ala Leu Asp Thr Asn Ser Gly Pro His  
 1 5 10

cag ata aga tct tgt gag ggt gat ggg att gac agg ttg gaa aaa tta 99  
 Gln Ile Arg Ser Cys Glu Gly Asp Gly Ile Asp Arg Leu Glu Lys Leu  
 15 20 25 30

agt att ggg ggc aga aag cag gag aaa gct ttg aga aat agg tgc ttt 147  
 Ser Ile Gly Gly Arg Lys Glu Lys Ala Leu Arg Asn Arg Cys Phe  
 35 40 45

ggt ggt aga gtt gct gca act aca caa tgt att ctt acc tca gat gct 195  
 Gly Gly Arg Val Ala Ala Thr Thr Gln Cys Ile Leu Thr Ser Asp Ala  
 50 55 60

tgt cct gaa act ctt cat tct caa aca cag tcc tct agg aaa aat tat 243  
 Cys Pro Glu Thr Leu His Ser Gln Thr Gln Ser Ser Arg Lys Asn Tyr  
 65 70 75

gct gat gca aac cgt gta tct gck atc att ttg ggc gga ggc act gga 291  
 Ala Asp Ala Asn Arg Val Ser Ala Ile Ile Leu Gly Gly Thr Gly  
 80 85 90

tct cag ctc ttt cct ctg aca agc aca aga gct acg cct gct gta cct 339  
 Ser Gln Leu Phe Pro Leu Thr Ser Thr Arg Ala Thr Pro Ala Val Pro  
 95 100 105 110

gtt gga gga tgt tac agg ctt att gat atc cct atg agt aac tgc ttc 387  
 Val Gly Gly Cys Tyr Arg Leu Ile Asp Ile Pro Met Ser Asn Cys Phe  
 115 120 125

aac agt ggt ata aat aag ata ttt gtg atg agt cag ttc aat tct act 435  
 Asn Ser Gly Ile Asn Lys Ile Phe Val Met Ser Gln Phe Asn Ser Thr  
 130 135 140

tcg ctt aac cgc cat att cat cgt aca tac ctt gaa ggc ggg atc aac 483

Ser Leu Asn Arg His Ile His Arg Thr Tyr Leu Glu Gly Gly Ile Asn  
 145 150 155  
 ttt gct gat gga tct gta cag gta tta gtc gct aca caa atg cct gaa 531  
 Phe Ala Asp Gly Ser Val Gln Val Leu Ala Ala Thr Gln Met Pro Glu  
 160 165 170  
 gag cca gct gga tgg ttc cag ggt aca gca gac tct atc aga aaa ttt 579  
 Glu Pro Ala Gly Trp Gln Gly Thr Ala Asp Ser Ile Arg Lys Phe  
 175 180 185 190  
 atc tgg gta ctc gag gat tat tac agt cac aaa tcc att gac aac att 627  
 Ile Trp Val Leu Glu Asp Tyr Tyr Ser His Lys Ser Ile Asp Asn Ile  
 195 200 205  
 gta atc ttg agt ggc gat cag ctt tat cgg atg aat tac atg gaa ctt 675  
 Val Ile Leu Ser Gly Asp Gln Leu Tyr Arg Met Asn Tyr Met Glu Leu  
 210 215 220  
 gtg cag aaa cat gtc gag gac gat gct gat atc act ata tca tgt gct 723  
 Val Gln Lys His Val Glu Asp Asp Ala Asp Ile Thr Ile Ser Cys Ala  
 225 230 235  
 cct gtt gat gag agc cga gct tct aaa aat ggg cta gtg aag att gat 771  
 Pro Val Asp Glu Ser Arg Ala Ser Lys Asn Gly Leu Val Lys Ile Asp  
 240 245 250  
 cat act gga cgt gta ctt caa ttc ttt gaa aaa cca aag ggt gct gat 819  
 His Thr Gly Arg Val Leu Gln Phe Phe Glu Lys Pro Lys Gly Ala Asp  
 255 260 265 270  
 ttg aat tct atg aga gtt gag acc aac ttc ctg agc tat gct ata gat 867  
 Leu Asn Ser Met Arg Val Glu Thr Asn Phe Leu Ser Tyr Ala Ile Asp  
 275 280 285  
 gat gca cag aaa tat cca tac ctt gca tca atg ggc att tat gtc ttc 915  
 Asp Ala Gln Lys Tyr Pro Tyr Leu Ala Ser Met Gly Ile Tyr Val Phe  
 290 295 300  
 aag aaa gat gca ctt tta gac ctt ctc aag tca aaa tat act caa tta 963  
 Lys Lys Asp Ala Leu Leu Asp Leu Leu Lys Ser Lys Tyr Thr Gln Leu  
 305 310 315  
 cat gac ttt gga tct gaa atc ctc cca aga gct gta cta gat cat agt 1011  
 His Asp Phe Gly Ser Glu Ile Leu Pro Arg Ala Val Leu Asp His Ser  
 320 325 330  
 gtg cag gca tgc att ttt acg ggc tat tgg gag gat gtt gga aca atc 1059  
 Val Gln Ala Cys Ile Phe Thr Gly Tyr Trp Glu Asp Val Gly Thr Ile  
 335 340 345 350  
 aaa tca ttc ttt gat gca aac ttg gcc ctc act gag cag cct tcc aag 1107  
 Lys Ser Phe Asp Ala Asn Leu Ala Leu Thr Glu Gln Pro Ser Lys  
 355 360 365  
 ttg gat ttt tac gat cca aaa aca cct ttc ttc act gca ccc cga tgc 1155  
 Phe Asp Phe Tyr Asp Pro Lys Thr Pro Phe Phe Thr Ala Pro Arg Cys

370	375	380	
ttg cct ccg acg caa ttg gac aag tgc aag atg aaa tat gca ttt atc Leu Pro Pro Thr Gln Leu Asp Lys Cys Lys Met Lys Tyr Ala Phe Ile 385 390 395			1203
tca gat ggt tgc tta ctg aga gaa tgc aac atc gag cat tct gtg att Ser Asp Gly Cys Leu Leu Arg Glu Cys Asn Ile Glu His Ser Val Ile 400 405 410			1251
gga gtc tgc tca cgt gtc agc tct gga tgt gaa ctc aag gac tcc gtg Gly Val Cys Ser Arg Val Ser Ser Gly Cys Glu Leu Lys Asp Ser Val 415 420 425 430			1299
atg atg gga gcg gac atc tat gaa act gaa gaa gaa gct tca aag cta Met Met Gly Ala Asp Ile Tyr Glu Thr Glu Glu Ala Ser Lys Leu 435 440 445			1347
ctg tta gct ggg aag gtc ccr gtt gga ata gga agg aac aca aag ata Leu Leu Ala Gly Lys Val Pro Val Gly Ile Gly Arg Asn Thr Lys Ile 450 455 460			1395
agg aac tgt atc att gac atg aat gct agg att ggg aag aac gtc gtg Arg Asn Cys Ile Ile Asp Met Asn Ala Arg Ile Gly Lys Asn Val Val 465 470 475			1443
atc aca aac agt aag ggc atc caa gag gct gat cac ccg gaa gaa ggg Ile Thr Asn Ser Lys Gly Ile Gln Glu Ala Asp His Pro Glu Glu Gly 480 485 490			1491
tac tcg tac tac ata agg tct gga atc gtg gtg atc ctg aag aat gca Tyr Ser Tyr Tyr Ile Arg Ser Gly Ile Val Val Ile Leu Lys Asn Ala 495 500 505 510			1539
acc atc aac gat ggg tct gtc ata tagatccgct gcgtktgcg Thr Ile Asn Asp Gly Ser Val Ile 515			1582
<210> 12			
<211> 518			
<212> PRT			
<213> Zea mays			
<400> 12			
Met Gln Phe Ala Leu Ala Leu Asp Thr Asn Ser Gly Pro His Gln Ile 1 5 10 15			
Arg Ser Cys Glu Gly Asp Gly Ile Asp Arg Leu Glu Lys Leu Ser Ile 20 25 30			
Gly Gly Arg Lys Gln Glu Lys Ala Leu Arg Asn Arg Cys Phe Gly Gly 35 40 45			
Arg Val Ala Ala Thr Thr Gln Cys Ile Leu Thr Ser Asp Ala Cys Pro 50 55 60			

Glu	Thr	Leu	His	Ser	Gln	Thr	Gln	Ser	Ser	Arg	Lys	Asn	Tyr	Ala	Asp
65										75					80
Ala	Asn	Arg	Val	Ser	Ala	Ile	Ile	Leu	Gly	Gly	Gly	Thr	Gly	Ser	Gln
			85					90						95	
Leu	Phe	Pro	Leu	Thr	Ser	Thr	Arg	Ala	Thr	Pro	Ala	Val	Pro	Val	Gly
			100				105						110		
Gly	Cys	Tyr	Arg	Leu	Ile	Asp	Ile	Pro	Met	Ser	Asn	Cys	Phe	Asn	Ser
	115					120						125			
Gly	Ile	Asn	Lys	Ile	Phe	Val	Met	Ser	Gln	Phe	Asn	Ser	Thr	Ser	Leu
	130					135					140				
Asn	Arg	His	Ile	His	Arg	Thr	Tyr	Leu	Glu	Gly	Gly	Ile	Asn	Phe	Ala
	145					150				155					160
Asp	Gly	Ser	Val	Gln	Val	Leu	Ala	Ala	Thr	Gln	Met	Pro	Glu	Glu	Pro
			165						170				175		
Ala	Gly	Trp	Phe	Gln	Gly	Thr	Ala	Asp	Ser	Ile	Arg	Lys	Phe	Ile	Trp
		180					185					190			
Val	Leu	Glu	Asp	Tyr	Tyr	Ser	His	Lys	Ser	Ile	Asp	Asn	Ile	Val	Ile
		195					200					205			
Leu	Ser	Gly	Asp	Gln	Leu	Tyr	Arg	Met	Asn	Tyr	Met	Glu	Leu	Val	Gln
		210				215					220				
Lys	His	Val	Glu	Asp	Asp	Ala	Asp	Ile	Thr	Ile	Ser	Cys	Ala	Pro	Val
	225					230				235			240		
Asp	Glu	Ser	Arg	Ala	Ser	Lys	Asn	Gly	Leu	Val	Lys	Ile	Asp	His	Thr
		245						250					255		
Gly	Arg	Val	Leu	Gln	Phe	Phe	Glu	Lys	Pro	Lys	Gly	Ala	Asp	Leu	Asn
		260				265					270				
Ser	Met	Arg	Val	Glu	Thr	Asn	Phe	Leu	Ser	Tyr	Ala	Ile	Asp	Asp	Ala
		275					280					285			
Gln	Lys	Tyr	Pro	Tyr	Leu	Ala	Ser	Met	Gly	Ile	Tyr	Val	Phe	Lys	Lys
		290				295					300				
Asp	Ala	Leu	Leu	Asp	Leu	Leu	Lys	Ser	Lys	Tyr	Thr	Gln	Leu	His	Asp
	305					310				315				320	
Phe	Gly	Ser	Glu	Ile	Leu	Pro	Arg	Ala	Val	Leu	Asp	His	Ser	Val	Gln
		325					330					335			
Ala	Cys	Ile	Phe	Thr	Gly	Tyr	Trp	Glu	Asp	Val	Gly	Thr	Ile	Lys	Ser
		340					345					350			
Phe	Phe	Asp	Ala	Asn	Leu	Ala	Leu	Thr	Glu	Gln	Pro	Ser	Lys	Phe	Asp
		355					360					365			

Phe Tyr Asp Pro Lys Thr Pro Phe Phe Thr Ala Pro Arg Cys Leu Pro  
 370 375 380

Pro Thr Gln Leu Asp Lys Cys Lys Met Lys Tyr Ala Phe Ile Ser Asp  
 385 390 395 400

Gly Cys Leu Leu Arg Glu Cys Asn Ile Glu His Ser Val Ile Gly Val  
 405 410 415

Cys Ser Arg Val Ser Ser Gly Cys Glu Leu Lys Asp Ser Val Met Met  
 420 425 430

Gly Ala Asp Ile Tyr Glu Thr Glu Glu Ala Ser Lys Leu Leu Leu  
 435 440 445

Ala Gly Lys Val Pro Val Gly Ile Gly Arg Asn Thr Lys Ile Arg Asn  
 450 455 460

Cys Ile Ile Asp Met Asn Ala Arg Ile Gly Lys Asn Val Val Ile Thr  
 465 470 475 480

Asn Ser Lys Gly Ile Gln Glu Ala Asp His Pro Glu Glu Gly Tyr Ser  
 485 490 495

Tyr Tyr Ile Arg Ser Gly Ile Val Val Ile Leu Lys Asn Ala Thr Ile  
 500 505 510

Asn Asp Gly Ser Val Ile  
 515

<210> 13  
 <211> 1582  
 <212> DNA  
 <213> Zea mays

<220>  
 <221> CDS  
 <222> (10)..(1563)  
 <223> Shrunken-2 gene revertant form, modified to be  
 heat stable

<220>  
 <221> variation  
 <222> (267)  
 <223> k = g or t; amino acid 86 = Ala.

<220>  
 <221> variation  
 <222> (1008)  
 <223> y = c or t.

<220>  
 <221> variation  
 <222> (1368)  
 <223> r = a or g; amino acid 453 = Pro.

<220>  
 <221> variation  
 <222> (1578)  
 <223> k = g or t.

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 ggaggagat atg cag ttt gca ctt gca ttg gac aac tca ggt cct cac 51  
 Met Gln Phe Ala Leu Ala Leu Asp Thr Asn Ser Gly Pro His  
 1 5 10  
 cag ata aga tct tgt gag ggt gat ggg att gac agg ttg gaa aaa tta 99  
 Gln Ile Arg Ser Cys Glu Gly Asp Gly Ile Asp Arg Leu Glu Lys Leu  
 15 20 25 30  
 agt att ggg ggc aga aag cag gag aaa gct ttg aga aat agg tgc ttt 147  
 Ser Ile Gly Gly Arg Lys Gln Glu Lys Ala Leu Arg Asn Arg Cys Phe  
 35 40 45  
 ggt ggt aga gtt gct gca act aca caa tgt att ctt acc tca gat gct 195  
 Gly Gly Arg Val Ala Ala Thr Thr Gln Cys Ile Leu Thr Ser Asp Ala  
 50 55 60  
 tgt cct gaa act ctt cat tct caa aca cag tcc tct agg aaa aat tat 243  
 Cys Pro Glu Thr Leu His Ser Gln Thr Gln Ser Ser Arg Lys Asn Tyr  
 65 70 75  
 gct gat gca aac cgt gta tct gck atc att ttg ggc gga ggc act gga 291  
 Ala Asp Ala Asn Arg Val Ala Ile Ile Leu Gly Gly Thr Gly  
 80 85 90  
 tct cag ctc ttt cct ctg aca agc aca aga gct acg cct gct gta cct 339  
 Ser Gln Leu Phe Pro Leu Thr Ser Thr Arg Ala Thr Pro Ala Val Pro  
 95 100 105 110  
 gtt gga gga tgt tac agg ctt att gat atc cct atg agt aac tgc ttc 387  
 Val Gly Gly Cys Tyr Arg Leu Ile Asp Ile Pro Met Ser Asn Cys Phe  
 115 120 125  
 aac agt ggt ata aat aag ata ttt gtg atg agt cag ttc aat tct act 435  
 Asn Ser Gly Ile Asn Lys Ile Phe Val Met Ser Gln Phe Asn Ser Thr  
 130 135 140  
 tcg ctt aac cgc cat att cat cgt aca tac ctt gaa ggc ggg atc aac 483  
 Ser Leu Asn Arg His Ile His Arg Thr Tyr Leu Glu Gly Ile Asn  
 145 150 155  
 ttg gct gat gga tct gta cag gta tta gcg gct aca caa atg cct gaa 531  
 Phe Ala Asp Gly Ser Val Gln Val Leu Ala Ala Thr Gln Met Pro Glu  
 160 165 170  
 gag cca gct gga tgg ttc cag ggt aca gca gac tct atc aga aaa ttt 579  
 Glu Pro Ala Gly Trp Phe Gln Gly Thr Ala Asp Ser Ile Arg Lys Phe  
 175 180 185 190  
 atc tgg gta ctc gag gat tat tac agt cac aaa tcc att gac aac att 627  
 Ile Trp Val Leu Glu Asp Tyr Tyr Ser His Lys Ser Ile Asn Ile

195	200	205	
gta atc ttg agt ggc gat cag ctt tat cggtatcataatgaa	ctt		675
Val Ile Leu Ser Gly Asp Gln Leu Tyr Arg Met Asn Tyr Met Glu Leu			
210	215	220	
gtg cag aaa cat gtc gag gac gat gct gat atc act ata tca tgt gct			723
Val Gln Lys His Val Glu Asp Asp Ala Asp Ile Thr Ile Ser Cys Ala			
225	230	235	
cct gtt gat gag agc cga gct tct aaa aat ggg cta gtg aag att gat			771
Pro Val Asp Glu Ser Arg Ala Ser Lys Asn Gly Leu Val Lys Ile Asp			
240	245	250	
cat act gga cgt gta ctt caa ttc ttt gaa aaa cca aag ggt gct gat			819
His Thr Gly Arg Val Leu Gln Phe Phe Glu Lys Pro Lys Gly Ala Asp			
255	260	265	270
ttg aat tct atg aga gtt gag acc aac ttc ctg agc tat gct ata gat			867
Leu Asn Ser Met Arg Val Glu Thr Asn Phe Leu Ser Tyr Ala Ile Asp			
275	280	285	
gat gca cag aaa tat cca tac ctt gca tca atg ggc att tat gtc ttc			915
Asp Ala Gln Lys Tyr Pro Tyr Leu Ala Ser Met Gly Ile Tyr Val Phe			
290	295	300	
aag aaa gat gca ctt tta gac ctt ctc aag tca aaa tat act caa tta			963
Lys Lys Asp Ala Leu Leu Asp Leu Leu Lys Ser Lys Tyr Thr Gln Leu			
305	310	315	
cat gac ttt gga tct gaa atc ctc cca aga gct gta cta gat tay agt			1011
His Asp Phe Gly Ser Glu Ile Leu Pro Arg Ala Val Leu Asp Tyr Ser			
320	325	330	
gtg cag gca tgc att ttt acg ggc tat tgg gag gat gtt gga aca atc			1059
Val Gln Ala Cys Ile Phe Thr Gly Tyr Trp Glu Asp Val Gly Thr Ile			
335	340	345	350
aaa tca ttc ttt gat gca aac ttg gcc ctc act gag cag cct tcc aag			1107
Lys Ser Phe Asp Ala Asn Leu Ala Leu Thr Glu Gln Pro Ser Lys			
355	360	365	
ttt gat ttt tac gat cca aaa aca cct ttc ttc act gca ccc cga tgc			1155
Phe Asp Phe Tyr Asp Pro Lys Thr Pro Phe Phe Thr Ala Pro Arg Cys			
370	375	380	
ttg cct ccg acg caa ttg gac aag atg aaa tat gca ttt atc			1203
Leu Pro Pro Thr Gln Leu Asp Lys Cys Lys Met Lys Tyr Ala Phe Ile			
385	390	395	
tca gat ggt tgc tta ctg aga gaa tgc aac atc gag cat tct gtg att			1251
Ser Asp Gly Cys Leu Leu Arg Glu Cys Asn Ile Glu His Ser Val Ile			
400	405	410	
gga gtc tgc tca cgt gtc agc tct gga aag gac tcc gtc gtg			1299
Gly Val Cys Ser Arg Val Ser Ser Gly Cys Glu Leu Lys Asp Ser Val			
415	420	425	430

atg atg gga gac atc tat gaa act gaa gaa gct tca aag cta Met Met Gly Ala Asp Ile Tyr Glu Thr Glu Glu Ala Ser Lys Leu 435 440 445	1347
ctg tta gct ggg aag gtc ccr gtt gga ata gga agg aac aca aag ata Leu Leu Ala Gly Lys Val Pro Val Gly Ile Gly Arg Asn Thr Lys Ile 450 455 460	1395
agg aac tgt atc att gac atg aat gct agg att ggg aag aac gtg gtg Arg Asn Cys Ile Ile Asp Met Asn Ala Arg Ile Gly Lys Asn Val Val 465 470 475	1443
atc aca aac agt aag ggc atc caa gag gct gat cac ccg gaa gaa ggg Ile Thr Asn Ser Lys Gly Ile Gln Glu Ala Asp His Pro Glu Glu Gly 480 485 490	1491
tac tcg tac tac ata agg tct gga atc gtg gtg atc ctg aag aat gca Tyr Ser Tyr Tyr Ile Arg Ser Gly Ile Val Val Ile Leu Lys Asn Ala 495 500 505 510	1539
acc atc aac gat ggg tct gtc ata tagatcgct gcgtktgcg Thr Ile Asn Asp Gly Ser Val Ile 515	1582

<210> 14  
<211> 518  
<212> PRT  
<213> Zea mays

<400> 14

Met Gln Phe Ala Leu Ala Leu Asp Thr Asn Ser Gly Pro His Gln Ile 1 5 10 15
Arg Ser Cys Glu Gly Asp Gly Ile Asp Arg Leu Glu Lys Leu Ser Ile 20 25 30
Gly Gly Arg Lys Gln Glu Lys Ala Leu Arg Asn Arg Cys Phe Gly Gly 35 40 45
Arg Val Ala Ala Thr Thr Gln Cys Ile Leu Thr Ser Asp Ala Cys Pro 50 55 60
Glu Thr Leu His Ser Gln Thr Gln Ser Ser Arg Lys Asn Tyr Ala Asp 65 70 75 80
Ala Asn Arg Val Ser Ala Ile Ile Leu Gly Gly Thr Gly Ser Gln 85 90 95
Leu Phe Pro Leu Thr Ser Thr Arg Ala Thr Pro Ala Val Pro Val Gly 100 105 110
Gly Cys Tyr Arg Leu Ile Asp Ile Pro Met Ser Asn Cys Phe Asn Ser 115 120 125

Gly Ile Asn Lys Ile Phe Val Met Ser Gln Phe Asn Ser Thr Ser Leu  
 130 135 140  
 Asn Arg His Ile His Arg Thr Tyr Leu Glu Gly Gly Ile Asn Phe Ala  
 145 150 155 160  
 Asp Gly Ser Val Gln Val Leu Ala Ala Thr Gln Met Pro Glu Glu Pro  
 165 170 175  
 Ala Gly Trp Phe Gln Gly Thr Ala Asp Ser Ile Arg Lys Phe Ile Trp  
 180 185 190  
 Val Leu Glu Asp Tyr Tyr Ser His Lys Ser Ile Asp Asn Ile Val Ile  
 195 200 205  
 Leu Ser Gly Asp Gln Leu Tyr Arg Met Asn Tyr Met Glu Leu Val Gln  
 210 215 220  
 Lys His Val Glu Asp Asp Ala Asp Ile Thr Ile Ser Cys Ala Pro Val  
 225 230 235 240  
 Asp Glu Ser Arg Ala Ser Lys Asn Gly Leu Val Lys Ile Asp His Thr  
 245 250 255  
 Gly Arg Val Leu Gln Phe Phe Glu Lys Pro Lys Gly Ala Asp Leu Asn  
 260 265 270  
 Ser Met Arg Val Glu Thr Asn Phe Leu Ser Tyr Ala Ile Asp Asp Ala  
 275 280 285  
 Gln Lys Tyr Pro Tyr Leu Ala Ser Met Gly Ile Tyr Val Phe Lys Lys  
 290 295 300  
 Asp Ala Leu Leu Asp Leu Leu Lys Ser Lys Tyr Thr Gln Leu His Asp  
 305 310 315 320  
 Phe Gly Ser Glu Ile Leu Pro Arg Ala Val Leu Asp Tyr Ser Val Gln  
 325 330 335  
 Ala Cys Ile Phe Thr Gly Tyr Trp Glu Asp Val Gly Thr Ile Lys Ser  
 340 345 350  
 Phe Phe Asp Ala Asn Leu Ala Leu Thr Glu Gln Pro Ser Lys Phe Asp  
 355 360 365  
 Phe Tyr Asp Pro Lys Thr Pro Phe Phe Thr Ala Pro Arg Cys Leu Pro  
 370 375 380  
 Pro Thr Gln Leu Asp Lys Cys Lys Met Lys Tyr Ala Phe Ile Ser Asp  
 385 390 395 400  
 Gly Cys Leu Leu Arg Glu Cys Asn Ile Glu His Ser Val Ile Gly Val  
 405 410 415  
 Cys Ser Arg Val Ser Ser Gly Cys Glu Leu Lys Asp Ser Val Met Met  
 420 425 430

Gly Ala Asp Ile Tyr Glu Thr Glu Glu Ala Ser Lys Leu Leu Leu  
 435 440 445

Ala Gly Lys Val Pro Val Gly Ile Gly Arg Asn Thr Lys Ile Arg Asn  
 450 455 460

Cys Ile Ile Asp Met Asn Ala Arg Ile Gly Lys Asn Val Val Ile Thr  
 465 470 475 480

Asn Ser Lys Gly Ile Gln Glu Ala Asp His Pro Glu Glu Gly Tyr Ser  
 485 490 495

Tyr Tyr Ile Arg Ser Gly Ile Val Val Ile Leu Lys Asn Ala Thr Ile  
 500 505 510

Asn Asp Gly Ser Val Ile  
 515

<210> 15  
<211> 1576  
<212> DNA  
<213> Zea mays

<220>  
<221> CDS  
<222> (10)..(1563)  
<223> Shrunken-2 gene revertant form, modified to be  
heat stable

<220>  
<221> variation  
<222> (267)  
<223> k = g or t; amino acid 86 = Ala.

<220>  
<221> variation  
<222> (1008)  
<223> y = c or t.

<220>  
<221> variation  
<222> (1368)  
<223> r = a or g; amino acid 453 = Pro.

<220>  
<221> variation  
<222> (1572)  
<223> k = g or t.

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ggaggagat atg cag ttt gca ctt gca ttg gac acg aac tca ggt cct cac 51  
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1 5 10

cag ata aga tct tgt gag ggt gat ggg att gac agg ttg gaa aaa tta 99  
Gln Ile Arg Ser Cys Glu Gly Asp Gly Ile Asp Arg Leu Glu Lys Leu

15	20	25	30	
agt att ggg ggc aga aag cag gag aaa gct ttg aga aat agg tgc ttt Ser Ile Gly Gly Arg Lys Gln Glu Lys Ala Leu Arg Asn Arg Cys Phe				147
35		40	45	
ggt ggt aga gtt gct gca act aca caa tgt att ctt acc tca gat gct Gly Gly Arg Val Ala Ala Thr Thr Gln Cys Ile Leu Thr Ser Asp Ala				195
50	55		60	
tgt cct gaa act ctt cat tct caa aca cag tcc tct agg aaa aat tat Cys Pro Glu Thr Leu His Ser Gln Thr Gln Ser Ser Arg Lys Asn Tyr				243
65	70		75	
gct gat gca aac cgt gta tct gck atc att ttg ggc gga ggc act gga Ala Asp Ala Asn Arg Val Ser Ala Ile Leu Gly Gly Gly Thr Gly				291
80	85	90		
tct cag ctc ttt cct ctg aca agc aca aga gct acg cct gct gta cct Ser Gln Leu Phe Pro Leu Thr Ser Thr Arg Ala Thr Pro Ala Val Pro				339
95	100	105	110	
gtt gga gga tgt tac agg ctt att gat atc cct atg agt aac tgc ttc Val Gly Gly Cys Tyr Arg Leu Ile Asp Pro Met Ser Asn Cys Phe				387
115		120	125	
aac agt ggt ata aat aag ata ttt gtg atg agt cag ttc aat tct act Asn Ser Gly Ile Asn Lys Ile Phe Val Met Ser Gln Phe Asn Ser Thr				435
130		135	140	
tcg ctt aac cgc cat att cat cgt aca tac ctt gaa ggc ggg atc aac Ser Leu Asn Arg His Ile His Arg Thr Tyr Leu Glu Gly Gly Ile Asn				483
145		150	155	
ttt gct gat gga tct gta cag gta tta gcg gct aca caa atg cct gaa Phe Ala Asp Gly Ser Val Gln Val Leu Ala Ala Thr Gln Met Pro Glu				531
160	165		170	
gag cca gct gga tgg ttc cag ggt aca gca gac tct atc aga aaa ttt Glu Pro Ala Gly Trp Phe Gln Gly Thr Ala Asp Ser Ile Arg Lys Phe				579
175	180	185	190	
atc tgg gta ctc gag gat tat tac agt cac aaa tcc att gac aac att Ile Trp Val Leu Glu Asp Tyr Tyr Ser His Lys Ser Ile Asp Asn Ile				627
195		200	205	
gta atc ttg agt ggc gat cag ctt tat cgg atg aat tac atg gaa ctt Val Ile Leu Ser Gly Asp Gln Leu Tyr Arg Met Asn Tyr Met Glu Leu				675
210		215	220	
gtg cag aaa cat gtc gag gac gat gct gat atc act ata tca tgt gct Val Gln Lys His Val Glu Asp Asp Ala Asp Ile Thr Ile Ser Cys Ala				723
225	230	235		
cct gtt gat gag agc cga gct tct aaa aat ggg cta gtg aag att gat Pro Val Asp Glu Ser Arg Ala Ser Lys Asn Gly Leu Val Lys Ile Asp				771
240	245	250		

cat act gga cgt gta ctt caa ttc ttt gaa aaa cca aag ggt gct gat His Thr Gly Arg Val Leu Gln Phe Phe Glu Lys Pro Lys Gly Ala Asp 255 260 265 270	819
ttg aat tct atg aga gtt gag acc aac ttc ctg agc tat gct ata gat Leu Asn Ser Met Arg Val Glu Thr Asn Phe Leu Ser Tyr Ala Ile Asp 275 280 285	867
gat gca cag aaa tat cca tac ctt gca tca atg ggc att tat gtc ttc Asp Ala Gln Lys Tyr Pro Tyr Leu Ala Ser Met Gly Ile Tyr Val Phe 290 295 300	915
aag aaa gat gca ctt tta gac ctt ctc aag tca aaa tat act caa tta Lys Lys Asp Ala Leu Leu Asp Leu Lys Ser Lys Tyr Thr Gln Leu 305 310 315	963
cat gac ttt gga tct gaa atc ctc cca aga gct gta cta gat tay agt His Asp Phe Gly Ser Glu Ile Leu Pro Arg Ala Val Leu Asp Tyr Ser 320 325 330	1011
gtg cag gca tgc att ttt acg ggc tat tgg gag gat gtt gga aca atc Val Gln Ala Cys Ile Phe Thr Gly Tyr Trp Glu Asp Val Gly Thr Ile 335 340 345 350	1059
aaa tca ttc ttt gat gca aac ttg gcc ctc act gag cag cct tcc aag Lys Ser Phe Asp Ala Asn Leu Ala Leu Thr Glu Gln Pro Ser Lys 355 360 365	1107
ttt gat ttt tac gat cca aaa aca cct ttc ttc act gca ccc cga tgc Phe Asp Tyr Asp Pro Lys Thr Pro Phe Phe Thr Ala Pro Arg Cys 370 375 380	1155
ttg cct ccg acg caa ttg gac aag tgc aag atg aaa tat gca ttt atc Leu Pro Pro Thr Gln Leu Asp Lys Cys Lys Met Lys Tyr Ala Phe Ile 385 390 395	1203
tca gat ggt tgc tta ctg aga gaa tgc aac atc gag cat tct gtg att Ser Asp Gly Cys Leu Leu Arg Glu Cys Asn Ile Glu His Ser Val Ile 400 405 410	1251
ggg gtc tgc tca cgt gtc agc tct gga tgt gaa aag ctc aag gac tcc gtg Gly Val Cys Ser Arg Val Ser Ser Gly Cys Glu Leu Lys Asp Ser Val 415 420 425 430	1299
atg atg gga gcg gac atc tat gaa act gaa gaa gaa gct tca aag cta Met Met Gly Ala Asp Ile Tyr Glu Thr Glu Glu Ala Ser Lys Leu 435 440 445	1347
ctg tta gct ggg aag gtc ccr gtt gga ata gga agg aac aca aag ata Leu Leu Ala Gly Lys Val Pro Val Gly Ile Gly Arg Asn Thr Lys Ile 450 455 460	1395
agg aac tgt atc att gac atg aat gct agg att ggg aag aac gtg gtg Arg Asn Cys Ile Ile Asp Met Asn Ala Arg Ile Gly Lys Asn Val Val 465 470 475	1443

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atc aca aac agt aag ggc atc caa gag gct gat cac ccg gaa gaa ggg 1491
Ile Thr Asn Ser Lys Gly Ile Gln Glu Ala Asp His Pro Glu Glu Gly
480          485          490

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tac tac ata agg tct gga atc gtg gtg atc ctg aag aat gca acc atc 1539
Tyr Tyr Ile Arg Ser Gly Ile Val Val Ile Leu Lys Asn Ala Thr Ile
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Gly Gly Arg Lys Gln Glu Lys Ala Leu Arg Asn Arg Cys Phe Gly Gly  
35 40 45

Arg Val Ala Ala Thr Thr Gln Cys Ile Leu Thr Ser Asp Ala Cys Pro  
50 55 60

Glu Thr Leu His Ser Gln Thr Gln Ser Ser Arg Lys Asn Tyr Ala Asp  
65 70 75 80

Ala Asn Arg Val Ser Ala Ile Ile Leu Gly Gly Gly Thr Gly Ser Gln  
85 90 95

Leu Phe Pro Leu Thr Ser Thr Arg Ala Thr Pro Ala Val Pro Val Gly  
100 105 110

Gly Cys Tyr Arg Leu Ile Asp Ile Pro Met Ser Asn Cys Phe Asn Ser  
115 120 125

Gly Ile Asn Lys Ile Phe Val Met Ser Gln Phe Asn Ser Thr Ser Leu  
130 135 140

Asn Arg His Ile His Arg Thr Tyr Leu Glu Gly Gly Ile Asn Phe Ala  
145 150 155 160

Asp Gly Ser Val Gln Val Leu Ala Ala Thr Gln Met Pro Glu Glu Pro  
165 170 175

Ala Gly Trp Phe Gln Gly Thr Ala Asp Ser Ile Arg Lys Phe Ile Trp  
180 185 190

Val Ile Glu Asp Tyr Tyr Ser His Iys Ser Ile Asp Asn Ile Val Ile

195	200	205
Leu Ser Gly Asp Gln Leu Tyr Arg Met Asn Tyr	Met Glu Leu Val Gln	
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Lys His Val Glu Asp Asp Ala Asp Ile Thr Ile Ser Cys Ala Pro Val		
225	230	235 240
Asp Glu Ser Arg Ala Ser Lys Asn Gly Leu Val Lys Ile Asp His Thr		
245	250	255
Gly Arg Val Leu Gln Phe Phe Glu Lys Pro Lys Gly Ala Asp Leu Asn		
260	265	270
Ser Met Arg Val Glu Thr Asn Phe Leu Ser Tyr Ala Ile Asp Asp Ala		
275	280	285
Gln Lys Tyr Pro Tyr Leu Ala Ser Met Gly Ile Tyr Val Phe Lys Lys		
290	295	300
Asp Ala Leu Leu Asp Leu Leu Lys Ser Lys Tyr Thr Gln Leu His Asp		
305	310	315 320
Phe Gly Ser Glu Ile Leu Pro Arg Ala Val Leu Asp Tyr Ser Val Gln		
325	330	335
Ala Cys Ile Phe Thr Gly Tyr Trp Glu Asp Val Gly Thr Ile Lys Ser		
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Phe Phe Asp Ala Asn Leu Ala Leu Thr Glu Gln Pro Ser Lys Phe Asp		
355	360	365
Phe Tyr Asp Pro Lys Thr Pro Phe Phe Thr Ala Pro Arg Cys Leu Pro		
370	375	380
Pro Thr Gln Leu Asp Lys Cys Lys Met Lys Tyr Ala Phe Ile Ser Asp		
385	390	395 400
Gly Cys Leu Leu Arg Glu Cys Asn Ile Glu His Ser Val Ile Gly Val		
405	410	415
Cys Ser Arg Val Ser Ser Gly Cys Glu Leu Lys Asp Ser Val Met Met		
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Gly Ala Asp Ile Tyr Glu Thr Glu Glu Ala Ser Lys Leu Leu Leu		
435	440	445
Ala Gly Lys Val Pro Val Gly Ile Gly Arg Asn Thr Lys Ile Arg Asn		
450	455	460
Cys Ile Ile Asp Met Asn Ala Arg Ile Gly Lys Asn Val Val Ile Thr		
465	470	475 480
Asn Ser Lys Gly Ile Gln Glu Ala Asp His Pro Glu Glu Gly Tyr Tyr		
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505

510

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<220>  
<221> CDS  
<222> (10)..(1563)  
<223> Shrunken-2 gene revertant form, modified to be  
heat stable

<220>  
<221> variation  
<222> (267)  
<223> k = g or t; amino acid 86 = Ala.

<220>  
<221> variation  
<222> (540)  
<223> n = a or g or c or t/u, unknown, or other.

<220>  
<221> variation  
<222> (1008)  
<223> y = c or t.

<220>  
<221> variation  
<222> (1368)  
<223> r = a or g; amino acid 453 = Pro.

<220>  
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<222> (1572)  
<223> k = g or t.

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cag ata aga tct tgt gag ggt gat ggg att gac agg ttg gaa aaa tta 99  
Gln Ile Arg Ser Cys Glu Gly Asp Gly Ile Asp Arg Leu Glu Lys Leu  
15 20 25 30

agt att ggg ggc aga aag cag gag aaa gct ttg aga aat agg tgc ttt 147  
Ser Ile Gly Gly Arg Lys Gln Glu Lys Ala Leu Arg Asn Arg Cys Phe  
35 40 45

ggt ggt aga gtt gct gca act aca caa tgt att ctt acc tca gat gct 195  
Gly Gly Arg Val Ala Ala Thr Thr Gln Cys Ile Leu Thr Ser Asp Ala

50	55	60	
tgt cct gaa act ctt cat tct caa aca cag tcc tct agg aaa aat tat Cys Pro Glu Thr Leu His Ser Gln Thr Gln Ser Ser Arg Lys Asn Tyr 65	70	75	243
gct gat gca aac cgt gta tct gck atc att ttg ggc gga ggc act gga Ala Asp Ala Asn Arg Val Ser Ala Ile Ile Leu Gly Gly Thr Gly 80	85	90	291
tct cag ctc ttt cct ctg aca agc aca aga gct acg cct gct gta cct Ser Gln Leu Phe Pro Leu Thr Ser Thr Arg Ala Thr Pro Ala Val Pro 95	100	105	339
gtt gga gga tgt tac agg ctt att gat atc cct atg agt aac tgc ttc Val Gly Gly Cys Tyr Arg Leu Ile Asp Ile Pro Met Ser Asn Cys Phe 115	120	125	387
aac agt ggt ata aat aag ata ttt gtg atg agt cag ttc aat tct act Asn Ser Gly Ile Asn Lys Ile Phe Val Met Ser Gln Phe Asn Ser Thr 130	135	140	435
tcg ctt aac cgc cat att cat cgt aca tac ctt gaa ggc ggg atc aac Ser Leu Asn Arg His Ile His Arg Thr Tyr Leu Glu Gly Ile Asn 145	150	155	483
ttt gct gat gga tct gta cag gta tta gcg gct aca caa atg cct gaa Phe Ala Asp Gly Ser Val Gln Val Leu Ala Ala Thr Gln Met Pro Glu 160	165	170	531
gag cca ccn gga tgg ttc cag ggt aca gca gac tct atc aga aaa ttt Glu Pro Pro Gly Trp Phe Gln Gly Thr Ala Asp Ser Ile Arg Lys Phe 175	180	185	579
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gta atc ttg agt ggc gat cag ctt tat cgg atg aat tac atg gaa ctt Val Ile Leu Ser Gly Asp Gln Leu Tyr Arg Met Asn Tyr Met Glu Leu 210	215	220	675
gtg cag aaa cat gtc gag gac gat gct gat atc act ata tca tgt gct Val Gln Lys His Val Glu Asp Asp Ala Asp Ile Thr Ile Ser Cys Ala 225	230	235	723
cct gtt gat gag agc cga gct tct aaa aat ggg cta gtg aag att gat Pro Val Asp Glu Ser Arg Ala Ser Lys Asn Gly Leu Val Lys Ile Asp 240	245	250	771
cat act gga cgt gta ctt caa ttc ttt gaa aaa cca aag ggt gct gat His Thr Gly Arg Val Leu Gln Phe Phe Glu Lys Pro Lys Gly Ala Asp 255	260	265	819
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305 310 315	
cat gac ttt gga tct gaa atc ctc cca aga gct gta cta gat cay agt His Asp Phe Gly Ser Glu Ile Leu Pro Arg Ala Val Leu Asp His Ser	1011
320 325 330	
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335 340 345 350	
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355 360 365	
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370 375 380	
ttg cct ccg acg caa ttg gac aag tgc aag atg aaa tat gca ttt atc Leu Pro Pro Thr Gln Leu Asp Lys Cys Lys Met Lys Tyr Ala Phe Ile	1203
385 390 395	
tca gat ggt tgc tta ctg aga gaa tgc aac atc gag cat tct gtg att Ser Asp Gly Cys Leu Leu Arg Glu Cys Asn Ile Glu His Ser Val Ile	1251
400 405 410	
gga gtc tgc tca cgt gtc agc tct gga tgt gaa ctc aag gac tcc gtg Gly Val Cys Ser Arg Val Ser Ser Gly Cys Glu Leu Lys Asp Ser Val	1299
415 420 425 430	
atg atg gga gcg gac atc tat gaa act gaa gaa gaa gct tca aag cta Met Met Gly Ala Asp Ile Tyr Glu Thr Glu Glu Ala Ser Lys Leu	1347
435 440 445	
ctg tta gct ggg aag gtc ccr gtt gga ata gga agg aac aca aag ata Leu Leu Ala Gly Lys Val Pro Val Gly Ile Gly Arg Asn Thr Lys Ile	1395
450 455 460	
agg aac tgt atc att gac atg aat gct agg att ggg aag aac gtg gtg Arg Asn Cys Ile Ile Asp Met Asn Ala Arg Ile Gly Lys Asn Val Val	1443
465 470 475	
atc aca aac agt aag ggc atc caa gag gct gat cac ccg gaa gaa ggg Ile Thr Asn Ser Lys Gly Ile Gln Glu Ala Asp His Pro Glu Glu Gly	1491
480 485 490	
tac tac ata agg tct gga atc gtg gtg atc ctg aag aat gca acc atc Tyr Tyr Ile Arg Ser Gly Ile Val Val Ile Leu Lys Asn Ala Thr Ile	1539
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 35 40 45  
 Arg Val Ala Ala Thr Thr Gln Cys Ile Leu Thr Ser Asp Ala Cys Pro  
 50 55 60  
 Glu Thr Leu His Ser Gln Thr Gln Ser Ser Arg Lys Asn Tyr Ala Asp  
 65 70 75 80  
 Ala Asn Arg Val Ser Ala Ile Ile Leu Gly Gly Thr Gly Ser Gln  
 85 90 95  
 Leu Phe Pro Leu Thr Ser Thr Arg Ala Thr Pro Ala Val Pro Val Gly  
 100 105 110  
 Gly Cys Tyr Arg Leu Ile Asp Ile Pro Met Ser Asn Cys Phe Asn Ser  
 115 120 125  
 Gly Ile Asn Lys Ile Phe Val Met Ser Gln Phe Asn Ser Thr Ser Leu  
 130 135 140  
 Asn Arg His Ile His Arg Thr Tyr Leu Glu Gly Gly Ile Asn Phe Ala  
 145 150 155 160  
 Asp Gly Ser Val Gln Val Leu Ala Ala Thr Gln Met Pro Glu Glu Pro  
 165 170 175  
 Pro Gly Trp Phe Gln Gly Thr Ala Asp Ser Ile Arg Lys Phe Ile Trp  
 180 185 190  
 Val Leu Glu Asp Tyr Tyr Ser His Lys Ser Ile Asp Asn Ile Val Ile  
 195 200 205  
 Leu Ser Gly Asp Gln Leu Tyr Arg Met Asn Tyr Met Glu Leu Val Gln  
 210 215 220  
 Lys His Val Glu Asp Asp Ala Asp Ile Thr Ile Ser Cys Ala Pro Val  
 225 230 235 240  
 Asp Glu Ser Arg Ala Ser Lys Asn Gly Leu Val Lys Ile Asp His Thr

245	250	255
Gly Arg Val Leu Gln Phe Phe Glu Lys Pro Lys Gly Ala Asp Leu Asn		
260	265	270
Ser Met Arg Val Glu Thr Asn Phe Leu Ser Tyr Ala Ile Asp Asp Ala		
275	280	285
Gln Lys Tyr Pro Tyr Leu Ala Ser Met Gly Ile Tyr Val Phe Lys Lys		
290	295	300
Asp Ala Leu Leu Asp Leu Leu Lys Ser Lys Tyr Thr Gln Leu His Asp		
305	310	315
Phe Gly Ser Glu Ile Leu Pro Arg Ala Val Leu Asp His Ser Val Gln		
325	330	335
Ala Cys Ile Phe Thr Gly Tyr Trp Glu Asp Val Gly Thr Ile Lys Ser		
340	345	350
Phe Phe Asp Ala Asn Leu Ala Leu Thr Glu Gln Pro Ser Lys Phe Asp		
355	360	365
Phe Tyr Asp Pro Lys Thr Pro Phe Phe Thr Ala Pro Arg Cys Leu Pro		
370	375	380
Pro Thr Gln Leu Asp Lys Cys Lys Met Lys Tyr Ala Phe Ile Ser Asp		
385	390	395
Gly Cys Leu Leu Arg Glu Cys Asn Ile Glu His Ser Val Ile Gly Val		
405	410	415
Cys Ser Arg Val Ser Ser Gly Cys Glu Leu Lys Asp Ser Val Met Met		
420	425	430
Gly Ala Asp Ile Tyr Glu Thr Glu Glu Ala Ser Lys Leu Leu Leu		
435	440	445
Ala Gly Lys Val Pro Val Gly Ile Gly Arg Asn Thr Lys Ile Arg Asn		
450	455	460
Cys Ile Ile Asp Met Asn Ala Arg Ile Gly Lys Asn Val Val Ile Thr		
465	470	475
Asn Ser Lys Gly Ile Gln Glu Ala Asp His Pro Glu Glu Gly Tyr Tyr		
485	490	495
Ile Arg Ser Gly Ile Val Val Ile Leu Lys Asn Ala Thr Ile Asn Asp		
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Gly Ser Val Ile		
515		

&lt;210&gt; 19

&lt;211&gt; 1576

&lt;212&gt; DNA

<213> Zea mays

<220>

<221> CDS

<222> (10)..(1563)

<223> Shrunken-2 gene revertant form, modified to be  
heat stable

<220>

<221> variation

<222> (267)

<223> k = g or t; amino acid 86 = Ala.

<220>

<221> variation

<222> (1008)

<223> y = c or t.

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<222> (1209)

<223> y = c or t.

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<222> (1368)

<223> r = a or g; amino acid 453 = Pro.

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<222> (1371)

<223> h = a or c or t/u.

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<222> (1572)

<223> k = g or t.

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 Gln Ile Arg Ser Cys Glu Gly Asp Gly Ile Asp Arg Leu Glu Lys Leu  
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agt att ggg ggc aga aag cag gag aaa gct ttg aga aat agg tgc ttt 147  
 Ser Ile Gly Arg Lys Gln Glu Lys Ala Leu Arg Asn Arg Cys Phe  
 35 40 45

ggt ggt aga gtt gct gca act aca caa tgt att ctt acc tca gat gct 195  
 Gly Gly Arg Val Ala Ala Thr Thr Gln Cys Ile Leu Thr Ser Asp Ala  
 50 55 60

tgt cct gaa act ctt cat tct caa aca cag tcc tct agg aaa aat tat 243  
 Cys Pro Glu Thr Leu His Ser Gln Thr Gln Ser Ser Arg Lys Asn Tyr

65	70	75	
gct gat gca aac cgt gta tct gck atc att ttg ggc gga ggc act gga Ala Asp Ala Asn Arg Val Ser Ala Ile Leu Gly Gly Gly Thr Gly	80	85	291
		90	
tct cag ctc ttt cct ctg aca agc aca aga gct acg cct gct gta cct Ser Gln Leu Phe Pro Leu Thr Ser Thr Arg Ala Thr Pro Ala Val Pro	95	100	339
		105	110
gtt gga gga tgt tac agg ctt att gat atc cct atg agt aac tgc ttc Val Gly Gly Cys Tyr Arg Leu Ile Asp Ile Pro Met Ser Asn Cys Phe	115	120	387
		125	
aac agt ggt ata aat aag ata ttt gtg atg agt cag ttc aat tct act Asn Ser Gly Ile Asn Lys Ile Phe Val Met Ser Gln Phe Asn Ser Thr	130	135	435
		140	
tcg ctt aac cgc cat att cat cgt aca tac ctt gaa ggc ggg atc aac Ser Leu Asn Arg His Ile His Arg Thr Tyr Leu Glu Gly Gly Ile Asn	145	150	483
		155	
ttt gct gat gga tct gta cag gta tta gcg gct aca caa atg cct gaa Phe Ala Asp Gly Ser Val Gln Val Leu Ala Ala Thr Gln Met Pro Glu	160	165	531
		170	
gag cca gct gga tgg ttc cag ggt aca gca gac tct atc aga aaa ttt Glu Pro Ala Gly Trp Phe Gln Gly Thr Ala Asp Ser Ile Arg Lys Phe	175	180	579
		185	190
atc tgg gta ctc gag gat tat tac agt cac aaa tcc att gac aac att Ile Trp Val Leu Glu Asp Tyr Tyr Ser His Lys Ser Ile Asp Asn Ile	195	200	627
		205	
gta atc ttg agt ggc gat cag ctt tat cgg atg aat tac atg gaa ctt Val Ile Leu Ser Gly Asp Gln Leu Tyr Arg Met Asn Tyr Met Glu Leu	210	215	675
		220	
gtg cag aaa cat gtc gag gac gat gct gat atc act ata tca tgt gct Val Gln Lys His Val Glu Asp Asp Ala Asp Ile Thr Ile Ser Cys Ala	225	230	723
		235	
cct gtt gat gag agc cga gct tct aaa aat ggg cta gtg aag att gat Pro Val Asp Glu Ser Arg Ala Ser Lys Asn Gly Leu Val Lys Ile Asp	240	245	771
		250	
cat act gga cgt gta ctt caa ttc ttt gaa aaa cca aag ggt gct gat His Thr Gly Arg Val Leu Gln Phe Phe Glu Lys Pro Lys Gly Ala Asp	255	260	819
		265	270
ttg aat tct atg aga gtt gag acc aac ttc ctg agc tat gct ata gat Leu Asn Ser Met Arg Val Glu Thr Asn Phe Leu Ser Tyr Ala Ile Asp	275	280	867
		285	
gat gca cag aaa tat cca tac ctt gca tca atg ggc att tat gtc ttc Asp Ala Gln Lys Tyr Pro Tyr Leu Ala Ser Met Gly Ile Tyr Val Phe	290	295	915
		300	

aag aaa gat gca ctt tta gac ctt ctc aag tca aaa tat act caa tta Lys Lys Asp Ala Leu Leu Asp Leu Leu Lys Ser Lys Tyr Thr Gln Leu 305 310 315	963
cat gac ttt gga tct gaa atc ctc cca aga gct gta cta gat cay agt His Asp Phe Gly Ser Glu Ile Leu Pro Arg Ala Val Leu Asp His Ser 320 325 330	1011
gtg cag gca tgc att ttt acg ggc tat tgg gag gat gtt gga aca atc Val Gln Ala Cys Ile Phe Thr Gly Tyr Trp Glu Asp Val Gly Thr Ile 335 340 345 350	1059
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ttt gat ttt tac gat cca aaa aca cct ttc ttc act gca ccc cga tgc Phe Asp Phe Tyr Asp Pro Lys Thr Pro Phe Phe Thr Ala Pro Arg Cys 370 375 380	1155
ttg cct ccg acg caa ttg gac aag tgc aag atg aaa tat gca ttt atc Leu Pro Pro Thr Gln Leu Asp Lys Cys Lys Met Lys Tyr Ala Phe Ile 385 390 395	1203
tca cay ggt tgc tta ctg aga gaa tgc aac atc gag cat tct gtg att Ser His Gly Cys Leu Leu Arg Glu Cys Asn Ile Glu His Ser Val Ile 400 405 410	1251
gga gtc tgc tca cgt gtc agc tct gga tgt gaa ctc aag gac tcc gtg Gly Val Cys Ser Arg Val Ser Ser Gly Cys Glu Leu Lys Asp Ser Val 415 420 425 430	1299
atg atg gga gcg gac atc tat gaa act gaa gaa gaa gct tca aag cta Met Met Gly Ala Asp Ile Tyr Glu Thr Glu Glu Ala Ser Lys Leu 435 440 445	1347
ctg tta gct ggg aag gtc ccr ath gga ata gga agg aac aca aag ata Leu Leu Ala Gly Lys Val Pro Ile Gly Ile Gly Arg Asn Thr Lys Ile 450 455 460	1395
agg aac tgt atc att gac atg aat gct agg att ggg aag aac gtg gtg Arg Asn Cys Ile Ile Asp Met Asn Ala Arg Ile Gly Lys Asn Val Val 465 470 475	1443
atc aca aac agt aag ggc atc caa gag gct gat cac ccg gaa gaa ggg Ile Thr Asn Ser Lys Gly Ile Gln Glu Ala Asp His Pro Glu Glu Gly 480 485 490	1491
tac tac ata agg tct gga atc gtg gtg atc ctg aag aat gca acc atc Tyr Tyr Ile Arg Ser Gly Ile Val Val Ile Leu Lys Asn Ala Thr Ile 495 500 505 510	1539
aac gat ggg tct gtc ata tagatcggt gcgtktgcg Asn Asp Gly Ser Val Ile 515	1576

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<212> PRT  
<213> Zea mays

<400> 20

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							20		25				30		
Gly	Gly	Arg	Lys	Gln	Glu	Lys	Ala	Leu	Arg	Asn	Arg	Cys	Phe	Gly	Gly
							35		40			45			
Arg	Val	Ala	Ala	Thr	Thr	Gln	Cys	Ile	Leu	Thr	Ser	Asp	Ala	Cys	Pro
							50		55			60			
Glu	Thr	Leu	His	Ser	Gln	Thr	Gln	Ser	Ser	Arg	Lys	Asn	Tyr	Ala	Asp
							65		70		75		80		
Ala	Asn	Arg	Val	Ser	Ala	Ile	Ile	Leu	Gly	Gly	Gly	Thr	Gly	Ser	Gln
							85		90			95			
Leu	Phe	Pro	Leu	Thr	Ser	Thr	Arg	Ala	Thr	Pro	Ala	Val	Pro	Val	Gly
							100		105			110			
Gly	Cys	Tyr	Arg	Leu	Ile	Asp	Ile	Pro	Met	Ser	Asn	Cys	Phe	Asn	Ser
							115		120			125			
Gly	Ile	Asn	Lys	Ile	Phe	Val	Met	Ser	Gln	Phe	Asn	Ser	Thr	Ser	Leu
							130		135			140			
Asn	Arg	His	Ile	His	Arg	Thr	Tyr	Leu	Glu	Gly	Ile	Asn	Phe	Ala	
							145		150		155		160		
Asp	Gly	Ser	Val	Gln	Val	Leu	Ala	Ala	Thr	Gln	Met	Pro	Glu	Pro	
							165		170			175			
Ala	Gly	Trp	Phe	Gln	Gly	Thr	Ala	Asp	Ser	Ile	Arg	Lys	Phe	Ile	Trp
							180		185			190			
Val	Leu	Glu	Asp	Tyr	Tyr	Ser	His	Lys	Ser	Ile	Asp	Asn	Ile	Val	Ile
							195		200			205			
Leu	Ser	Gly	Asp	Gln	Leu	Tyr	Arg	Met	Asn	Tyr	Met	Glu	Leu	Val	Gln
							210		215			220			
Lys	His	Val	Glu	Asp	Asp	Ala	Asp	Ile	Thr	Ile	Ser	Cys	Ala	Pro	Val
							225		230		235		240		
Asp	Glu	Ser	Arg	Ala	Ser	Lys	Asn	Gly	Leu	Val	Lys	Ile	Asp	His	Thr
							245		250			255			
Gly	Arg	Val	Leu	Gln	Phe	Phe	Glu	Lys	Pro	Lys	Gly	Ala	Asp	Leu	Asn

260

265

270

Ser Met Arg Val Glu Thr Asn Phe Leu Ser Tyr Ala Ile Asp Asp Ala  
 275 280 285

Gln Lys Tyr Pro Tyr Leu Ala Ser Met Gly Ile Tyr Val Phe Lys Lys  
 290 295 300

Asp Ala Leu Leu Asp Leu Leu Lys Ser Lys Tyr Thr Gln Leu His Asp  
 305 310 315 320

Phe Gly Ser Glu Ile Leu Pro Arg Ala Val Leu Asp His Ser Val Gln  
 325 330 335

Ala Cys Ile Phe Thr Gly Tyr Trp Glu Asp Val Gly Thr Ile Lys Ser  
 340 345 350

Phe Phe Asp Ala Asn Leu Ala Leu Thr Glu Gln Pro Ser Lys Phe Asp  
 355 360 365

Phe Tyr Asp Pro Lys Thr Pro Phe Thr Ala Pro Arg Cys Leu Pro  
 370 375 380

Pro Thr Gln Leu Asp Lys Cys Lys Met Lys Tyr Ala Phe Ile Ser His  
 385 390 395 400

Gly Cys Leu Leu Arg Glu Cys Asn Ile Glu His Ser Val Ile Gly Val  
 405 410 415

Cys Ser Arg Val Ser Ser Gly Cys Glu Leu Lys Asp Ser Val Met Met  
 420 425 430

Gly Ala Asp Ile Tyr Glu Thr Glu Glu Ala Ser Lys Leu Leu Leu  
 435 440 445

Ala Gly Lys Val Pro Ile Gly Ile Gly Arg Asn Thr Lys Ile Arg Asn  
 450 455 460

Cys Ile Ile Asp Met Asn Ala Arg Ile Gly Lys Asn Val Val Ile Thr  
 465 470 475 480

Asn Ser Lys Gly Ile Gln Glu Ala Asp His Pro Glu Glu Gly Tyr Tyr  
 485 490 495

Ile Arg Ser Gly Ile Val Val Ile Leu Lys Asn Ala Thr Ile Asn Asp  
 500 505 510

Gly Ser Val Ile  
 515

&lt;210&gt; 21

&lt;211&gt; 1576

&lt;212&gt; DNA

&lt;213&gt; Zea mays

&lt;220&gt;

<221> CDS  
 <222> (10) ..(1563)  
 <223> Shrunken-2 gene revertant form, modified to be  
 heat stable

<220>  
 <221> variation  
 <222> (267)  
 <223> k = g or t; amino acid 86 = Ala.

<220>  
 <221> variation  
 <222> (321)  
 <223> n = a or g or c or t/u, unknown, or other.

<220>  
 <221> variation  
 <222> (1008)  
 <223> y = c or t.

<220>  
 <221> variation  
 <222> (1368)  
 <223> r = a or g; amino acid 453 = Pro.

<220>  
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 <222> (1572)  
 <223> k = g or t.

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 ggaggagat atg cag ttt gca ctt gca ttg gac acg aac tca ggt cct cac 51  
 Met Gln Phe Ala Leu Ala Leu Asp Thr Asn Ser Gly Pro His  
 1                       5                       10

cag ata aga tct tgt gag ggt gat ggg att gac agg ttg gaa aaa tta     99  
 Gln Ile Arg Ser Cys Glu Gly Asp Gly Ile Asp Arg Leu Glu Lys Leu  
 15                      20                      25                       30

agt att ggg ggc aga aag cag gag aaa gct ttg aga aat agg tgc ttt   147  
 Ser Ile Gly Gly Arg Lys Gln Glu Lys Ala Leu Arg Asn Arg Cys Phe  
 35                      40                      45

ggt ggt aga gtt gct gca act aca caa tgt att ctt acc tca gat gct   195  
 Gly Gly Arg Val Ala Ala Thr Thr Gln Cys Ile Leu Thr Ser Asp Ala  
 50                      55                      60

tgt cct gaa act ctt cat tct caa aca cag tcc tct agg aaa aat tat   243  
 Cys Pro Glu Thr Leu His Ser Gln Thr Gln Ser Ser Arg Lys Asn Tyr  
 65                      70                      75

gct gat gca aac cgt gta tct gck atc att ttg ggc gga ggc act gga   291  
 Ala Asp Ala Asn Arg Val Ser Ala Ile Ile Leu Gly Gly Gly Thr Gly  
 80                      85                      90

tct cag ctc ttt cct ctg aca agc aca acn gct acg cct gct gta cct   339  
 Ser Gln Leu Phe Pro Leu Thr Ser Thr Thr Ala Thr Pro Ala Val Pro

95	100	105	110	
gtt gga tgg tac agg ctt att gat atc cct atg agt aac tgc ttc Val Gly Gly Cys Tyr Arg Leu Ile Asp Ile Pro Met Ser Asn Cys Phe				387
115	120		125	
aac agt ggt ata aat aag ata ttt gtg atg agt cag ttc aat tct act Asn Ser Gly Ile Asn Lys Ile Phe Val Met Ser Gln Phe Asn Ser Thr				435
130	135		140	
tcg ctt aac cgc cat att cat cgt aca tac ctt gaa ggc ggg atc aac Ser Leu Asn Arg His Ile His Arg Thr Tyr Leu Glu Gly Gly Ile Asn				483
145	150		155	
ttt gct gat gga tct gta cag tta gcg gct aca caa atg cct gaa Phe Ala Asp Gly Ser Val Gln Val Leu Ala Ala Thr Gln Met Pro Glu				531
160	165		170	
gag cca gct gga tgg ttc cag ggt aca gca gac tct atc aga aaa ttt Glu Pro Ala Gly Trp Phe Gln Gly Thr Ala Asp Ser Ile Arg Lys Phe				579
175	180		185	
atc tgg gta ctc gag gat tat tac agt cac aaa tcc att gac aac att Ile Trp Val Leu Glu Asp Tyr Tyr Ser His Lys Ser Ile Asp Asn Ile				627
195	200		205	
gtc atc ttg agt ggc gat cag ctt tat cgg atg aat tac atg gaa ctt Val Ile Leu Ser Gly Asp Gln Leu Tyr Arg Met Asn Tyr Met Glu Leu				675
210	215		220	
gtg cag aaa cat gtc gag gac gat gct gat atc act ata tca tgt gct Val Gln Lys His Val Glu Asp Asp Ala Asp Ile Thr Ile Ser Cys Ala				723
225	230		235	
cct gtt gat gag agc cga gct tct aaa aat ggg cta gtg aag att gat Pro Val Asp Glu Ser Arg Ala Ser Lys Asn Gly Leu Val Lys Ile Asp				771
240	245		250	
cat act gga cgt gta ctt caa ttc ttt gaa aaa cca aag ggt gct gat His Thr Gly Arg Val Leu Gln Phe Phe Glu Lys Pro Lys Gly Ala Asp				819
255	260		265	
ttg aat tct atg aga gtt gag acc aac ttc ctg agc tat gct ata gat Leu Asn Ser Met Arg Val Glu Thr Asn Phe Leu Ser Tyr Ala Ile Asp				867
275	280		285	
gat gca cag aaa tat cca tac ctt gca tca atg ggc att tat gtc ttc Asp Ala Gln Lys Tyr Pro Tyr Leu Ala Ser Met Gly Ile Tyr Val Phe				915
290	295		300	
aag aaa gat gca ctt tta gac ctt ctc aag tca aaa tat act caa tta Lys Lys Asp Ala Leu Leu Asp Leu Leu Lys Ser Lys Tyr Thr Gln Leu				963
305	310		315	
cat gac ttt gga tct gaa atc ctc cca aga gct gta cta gat cay agt His Asp Phe Gly Ser Glu Ile Leu Pro Arg Ala Val Leu Asp His Ser				1011
320	325		330	

gtg cag gca tgc att ttt acg ggc tat tgg gag gat gtt gga aca atc Val Gln Ala Cys Ile Phe Thr Gly Tyr Trp Glu Asp Val Gly Thr Ile 335 340 345 350	1059
aaa tca ttc ttt gat gca aac ttg gcc ctc act gag cag cct tcc aag Lys Ser Phe Asp Ala Asn Leu Ala Leu Thr Glu Gln Pro Ser Lys 355 360 365	1107
ttt gat ttt tac gat cca aaa aca cct ttc ttc act gca ccc cga tgc Phe Asp Phe Tyr Asp Pro Lys Thr Pro Phe Thr Ala Pro Arg Cys 370 375 380	1155
ttg cct ccg acg caa ttg gac aag tgc aag atg aaa tat gca ttt atc Leu Pro Pro Thr Gln Leu Asp Lys Cys Lys Met Lys Tyr Ala Phe Ile 385 390 395	1203
tca gat ggt tgc tta ctg aga gaa tgc aac atc gag cat tct gtg att Ser Asp Gly Cys Leu Leu Arg Glu Cys Asn Ile Glu His Ser Val Ile 400 405 410	1251
gga gtc tgc tca cgt gtc agc tct gga tgt gaa ctc aag gac tcc gtg Gly Val Cys Ser Arg Val Ser Ser Gly Cys Glu Leu Lys Asp Ser Val 415 420 425 430	1299
atg atg gga gcg gac atc tat gaa act gaa gaa gaa gct tca aag cta Met Met Gly Ala Asp Ile Tyr Glu Thr Glu Glu Ala Ser Lys Leu 435 440 445	1347
ctg tta gct ggg aag gtc ccr gtt gga ata gga agg aac aca aag ata Leu Leu Ala Gly Lys Val Pro Val Gly Ile Gly Arg Asn Thr Lys Ile 450 455 460	1395
agg aac tgt atc att gac atg aat gct agg att ggg aag aac gtc gtg Arg Asn Cys Ile Ile Asp Met Asn Ala Arg Ile Gly Lys Asn Val Val 465 470 475	1443
atc aca aac agt aag ggc atc caa gag gct gat cac ccg gaa gaa ggg Ile Thr Asn Ser Lys Gly Ile Gln Glu Ala Asp His Pro Glu Glu Gly 480 485 490	1491
tac tac ata agg tct gga atc gtg gtg atc ctg aag aat gca acc atc Tyr Tyr Ile Arg Ser Gly Ile Val Val Ile Leu Lys Asn Ala Thr Ile 495 500 505 510	1539
aac gat ggg tct gtc ata tagatcggt gcgtktgcg Asn Asp Gly Ser Val Ile 515	1576
<210> 22 <211> 516 <212> PRT <213> Zea mays	
<400> 22	

Met Gln Phe Ala Leu Ala Leu Asp Thr Asn Ser Gly Pro His Gln Ile  
 1 5 10 15

Arg Ser Cys Glu Gly Asp Gly Ile Asp Arg Leu Glu Lys Leu Ser Ile  
 20 25 30

Gly Gly Arg Lys Gln Glu Lys Ala Leu Arg Asn Arg Cys Phe Gly Gly  
 35 40 45

Arg Val Ala Ala Thr Thr Gln Cys Ile Leu Thr Ser Asp Ala Cys Pro  
 50 55 60

Glu Thr Leu His Ser Gln Thr Gln Ser Ser Arg Lys Asn Tyr Ala Asp  
 65 70 75 80

Ala Asn Arg Val Ser Ala Ile Ile Leu Gly Gly Gly Thr Gly Ser Gln  
 85 90 95

Leu Phe Pro Leu Thr Ser Thr Thr Ala Thr Pro Ala Val Pro Val Gly  
 100 105 110

Gly Cys Tyr Arg Leu Ile Asp Ile Pro Met Ser Asn Cys Phe Asn Ser  
 115 120 125

Gly Ile Asn Lys Ile Phe Val Met Ser Gln Phe Asn Ser Thr Ser Leu  
 130 135 140

Asn Arg His Ile His Arg Thr Tyr Leu Glu Gly Gly Ile Asn Phe Ala  
 145 150 155 160

Asp Gly Ser Val Gln Val Leu Ala Ala Thr Gln Met Pro Glu Glu Pro  
 165 170 175

Ala Gly Trp Phe Gln Gly Thr Ala Asp Ser Ile Arg Lys Phe Ile Trp  
 180 185 190

Val Leu Glu Asp Tyr Tyr Ser His Lys Ser Ile Asp Asn Ile Val Ile  
 195 200 205

Leu Ser Gly Asp Gln Leu Tyr Arg Met Asn Tyr Met Glu Leu Val Gln  
 210 215 220

Lys His Val Glu Asp Asp Ala Asp Ile Thr Ile Ser Cys Ala Pro Val  
 225 230 235 240

Asp Glu Ser Arg Ala Ser Lys Asn Gly Leu Val Lys Ile Asp His Thr  
 245 250 255

Gly Arg Val Leu Gln Phe Phe Glu Lys Pro Lys Gly Ala Asp Leu Asn  
 260 265 270

Ser Met Arg Val Glu Thr Asn Phe Leu Ser Tyr Ala Ile Asp Asp Ala  
 275 280 285

Gln Lys Tyr Pro Tyr Leu Ala Ser Met Gly Ile Tyr Val Phe Lys Lys  
 290 295 300

Asp Ala Leu Leu Asp Leu Leu Lys Ser Lys Tyr Thr Gln Leu His Asp  
 305 310 315 320  
 Phe Gly Ser Glu Ile Leu Pro Arg Ala Val Leu Asp His Ser Val Gln  
 325 330 335  
 Ala Cys Ile Phe Thr Gly Tyr Trp Glu Asp Val Gly Thr Ile Lys Ser  
 340 345 350  
 Phe Phe Asp Ala Asn Leu Ala Leu Thr Glu Gln Pro Ser Lys Phe Asp  
 355 360 365  
 Phe Tyr Asp Pro Lys Thr Pro Phe Phe Thr Ala Pro Arg Cys Leu Pro  
 370 375 380  
 Pro Thr Gln Leu Asp Lys Cys Lys Met Lys Tyr Ala Phe Ile Ser Asp  
 385 390 395 400  
 Gly Cys Leu Leu Arg Glu Cys Asn Ile Glu His Ser Val Ile Gly Val  
 405 410 415  
 Cys Ser Arg Val Ser Ser Gly Cys Glu Leu Lys Asp Ser Val Met Met  
 420 425 430  
 Gly Ala Asp Ile Tyr Glu Thr Glu Glu Ala Ser Lys Leu Leu Leu  
 435 440 445  
 Ala Gly Lys Val Pro Val Gly Ile Gly Arg Asn Thr Lys Ile Arg Asn  
 450 455 460  
 Cys Ile Ile Asp Met Asn Ala Arg Ile Gly Lys Asn Val Val Ile Thr  
 465 470 475 480  
 Asn Ser Lys Gly Ile Gln Glu Ala Asp His Pro Glu Glu Gly Tyr Tyr  
 485 490 495  
 Ile Arg Ser Gly Ile Val Val Ile Leu Lys Asn Ala Thr Ile Asn Asp  
 500 505 510  
 Gly Ser Val Ile  
 515

<210> 23  
 <211> 1576  
 <212> DNA  
 <213> Zea mays

<220>  
 <221> CDS  
 <222> (10)..(1563)  
 <223> Shrunken-2 gene revertant form, modified to be  
 heat stable

<220>  
 <221> variation  
 <222> (267)

<223> k = g or t; amino acid 86 = Ala.

<220>  
<221> variation  
<222> (1008)  
<223> y = c or t.

<220>  
<221> variation  
<222> (1368)  
<223> r = a or g; amino acid 453 = Pro.

<220>  
<221> variation  
<222> (1389)  
<223> h = a or c or t/u.

<220>  
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<223> k = g or t.

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Met Gln Phe Ala Leu Ala Leu Asp Thr Asn Ser Gly Pro His  
1 5 10

cag ata aga tct tgt gag ggt gat ggg att gac agg ttg gaa aaa tta 99  
Gln Ile Arg Ser Cys Glu Gly Asp Gly Ile Asp Arg Leu Glu Lys Leu  
15 20 25 30

agt att ggg ggc aga aag cag gag aaa gct ttg aga aat agg tgc ttt 147  
Ser Ile Gly Gly Arg Lys Gln Glu Lys Ala Leu Arg Asn Arg Cys Phe  
35 40 45

ggt ggt aga gtt gct gca act aca caa tgt att ctt acc tca gat gct 195  
Gly Gly Arg Val Ala Ala Thr Thr Gln Cys Ile Leu Thr Ser Asp Ala  
50 55 60

tgt cct gaa act ctt cat tct caa aca cag tcc tct agg aaa aat tat 243  
Cys Pro Glu Thr Leu His Ser Gln Thr Gln Ser Ser Arg Lys Asn Tyr  
65 70 75

gct gat gca aac cgt gta tct gck atc att ttg ggc gga ggc act gga 291  
Ala Asp Ala Asn Arg Val Ser Ala Ile Ile Leu Gly Gly Thr Gly  
80 85 90

tct cag ctc ttt cct ctg aca agc aca aga gct acg cct gct gta cct 339  
Ser Gln Leu Phe Pro Leu Thr Ser Thr Arg Ala Thr Pro Ala Val Pro  
95 100 105 110

gtt gga gga tgt tac agg ctt att gat atc cct atg agt aac tgc ttc 387  
Val Gly Gly Cys Tyr Arg Leu Ile Asp Ile Pro Met Ser Asn Cys Phe  
115 120 125

aac agt ggt ata aat aag ata ttt gtg atg agt cag ttc aat tct act 435  
Asn Ser Gly Ile Asn Lys Ile Phe Val Met Ser Gln Phe Asn Ser Thr

130	135	140	
tcg ctt aac cgc cat att cat cgt aca tac ctt gaa ggc ggg atc aac Ser Leu Asn Arg His Ile His Arg Thr Tyr Leu Glu Gly Gly Ile Asn 145	150	155	483
ttt gct gat gga tct gta cag gta tta gcg gct aca caa atg cct gaa Phe Ala Asp Gly Ser Val Gln Val Leu Ala Ala Thr Gln Met Pro Glu 160	165	170	531
gag cca gct gga tgg ttc cag ggt aca gca gac tct atc aga aaa ttt Glu Pro Ala Gly Trp Phe Gln Gly Thr Ala Asp Ser Ile Arg Lys Phe 175	180	185	579
atc tgg gta ctc gag gat tat tac agt cac aaa tcc att gac aac att Ile Trp Val Leu Glu Asp Tyr Tyr Ser His Lys Ser Ile Asp Asn Ile 195	200	205	627
gta atc ttg agt ggc gat cag ctt tat cgg atg aat tac atg gaa ctt Val Ile Leu Ser Gly Asp Gln Leu Tyr Arg Met Asn Tyr Met Glu Leu 210	215	220	675
gtg cag aaa cat gtc gag gac gat gct gat atc act ata tca tgt gct Val Gln Ths His Val Glu Asp Ala Asp Ile Thr Ile Ser Cys Ala 225	230	235	723
cct gtt gat gag agc cga gct tct aaa aat ggg cta stg aag att gat Pro Val Asp Glu Ser Arg Ala Ser Lys Asn Gly Leu Val Lys Ile Asp 240	245	250	771
cat act gga cgt gta ctt caa ttc ttt gaa aaa cca aag ggt gct gat His Thr Gly Arg Val Leu Gln Phe Phe Glu Lys Pro Lys Gly Ala Asp 255	260	265	819
ttg aat tct atg aga gtt gag acc aac ttc ctg agc tat gct ata gat Leu Asn Ser Met Arg Val Glu Thr Asn Phe Leu Ser Tyr Ala Ile Asp 275	280	285	867
gat gca cag aaa tat cca tac ctt gca tca atg ggc att tat gtc ttc Asp Ala Gln Lys Tyr Pro Tyr Leu Ala Ser Met Gly Ile Tyr Val Phe 290	295	300	915
aag aaa gat gca ctt tta gac ctt ctc aag tca aaa tat act caa tta Lys Lys Asp Ala Leu Leu Asp Leu Leu Lys Ser Lys Tyr Thr Gln Leu 305	310	315	963
cat gac ttt gga tct gaa atc ctc cca aga gct gta cta gat tay agt His Asp Phe Gly Ser Glu Ile Leu Pro Arg Ala Val Leu Asp Tyr Ser 320	325	330	1011
gtg cag gca tgc att ttt acg ggc tat tgg gag gat gtt gga aca atc Val Gln Ala Cys Ile Phe Thr Gly Tyr Trp Glu Asp Val Gly Thr Ile 335	340	345	1059
aaa tca ttc ttt gat gca aac ttg gcc ctc act gag cag cct tcc aag Lys Ser Phe Phe Asp Ala Asn Leu Ala Leu Thr Glu Gln Pro Ser Lys 355	360	365	1107

ttt gat ttt tac gat cca aaa aca cct ttc ttc act gca ccc cga tgc 1155  
 Phe Asp Phe Tyr Asp Pro Lys Thr Pro Phe Phe Thr Ala Pro Arg Cys  
 370 375 380

ttg cct ccg acg caa ttg gac aag tgc aag atg aaa tat gca ttt atc 1203  
 Leu Pro Pro Thr Gln Leu Asp Lys Cys Lys Met Lys Tyr Ala Phe Ile  
 385 390 395

tca gat ggt tgc tta ctg aga gaa tgc aac atc gag cat tct gtg att 1251  
 Ser Asp Gly Cys Leu Leu Arg Glu Cys Asn Ile Glu His Ser Val Ile  
 400 405 410

gga gtc tgc tca cgt gtc agc tct gga tgt gaa ctc aag gac tcc gtg 1299  
 Gly Val Cys Ser Arg Val Ser Ser Gly Cys Glu Leu Lys Asp Ser Val  
 415 420 425 430

atg atg gga gcg gac atc tat gaa act gaa gaa gct tca aag cta 1347  
 Met Met Gly Ala Asp Ile Tyr Glu Thr Glu Glu Ala Ser Lys Leu  
 435 440 445

ctg tta gct ggg aag gtc ccr gtt gga ata gga agg aac ath aag ata 1395  
 Leu Leu Ala Gly Lys Val Pro Val Gly Ile Gly Arg Asn Ile Lys Ile  
 450 455 460

agg aac tgt atc att gac atg aat gct agg att ggg aag aac gtg gtg 1443  
 Arg Asn Cys Ile Ile Asp Met Asn Ala Arg Ile Gly Lys Asn Val Val  
 465 470 475

atc aca aac agt aag ggc atc caa gag gct gat cac ccg gaa gaa ggg 1491  
 Ile Thr Asn Ser Lys Gly Ile Gln Glu Ala Asp His Pro Glu Glu Gly  
 480 485 490

tac tac ata agg tct gga atc gtg gtg atc ctg aag aat gca acc atc 1539  
 Tyr Tyr Ile Arg Ser Gly Ile Val Val Ile Leu Lys Asn Ala Thr Ile  
 495 500 505 510

aac gat ggg tct gtc ata tagatcggt gcgtktgcg 1576  
 Asn Asp Gly Ser Val Ile  
 515

<210> 24  
<211> 516  
<212> PRT  
<213> Zea mays

<400> 24

Met Gln Phe Ala Leu Ala Leu Asp Thr Asn Ser Gly Pro His Gln Ile  
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Arg Ser Cys Glu Gly Asp Gly Ile Asp Arg Leu Glu Lys Leu Ser Ile  
 20 25 30

Gly Gly Arg Lys Gln Glu Lys Ala Leu Arg Asn Arg Cys Phe Gly Gly  
 35 40 45

Arg	Val	Ala	Ala	Thr	Thr	Gln	Cys	Ile	Leu	Thr	Ser	Asp	Ala	Cys	Pro
50						55						60			
Glu	Thr	Leu	His	Ser	Gln	Thr	Gln	Ser	Ser	Arg	Lys	Asn	Tyr	Ala	Asp
65					70					75				80	
Ala	Asn	Arg	Val	Ser	Ala	Ile	Ile	Leu	Gly	Gly	Gly	Thr	Gly	Ser	Gln
				85				90				95			
Leu	Phe	Pro	Leu	Thr	Ser	Thr	Arg	Ala	Thr	Pro	Ala	Val	Pro	Val	Gly
				100			105					110			
Gly	Cys	Tyr	Arg	Leu	Ile	Asp	Ile	Pro	Met	Ser	Asn	Cys	Phe	Asn	Ser
				115			120				125				
Gly	Ile	Asn	Lys	Ile	Phe	Val	Met	Ser	Gln	Phe	Asn	Ser	Thr	Ser	Leu
				130			135			140					
Asn	Arg	His	Ile	His	Arg	Thr	Tyr	Leu	Glu	Gly	Gly	Ile	Asn	Phe	Ala
145					150				155				160		
Asp	Gly	Ser	Val	Gln	Val	Leu	Ala	Ala	Thr	Gln	Met	Pro	Glu	Glu	Pro
					165				170				175		
Ala	Gly	Trp	Phe	Gln	Gly	Thr	Ala	Asp	Ser	Ile	Arg	Lys	Phe	Ile	Trp
				180			185				190				
Val	Leu	Glu	Asp	Tyr	Tyr	Ser	His	Lys	Ser	Ile	Asp	Asn	Ile	Val	Ile
				195			200			205					
Leu	Ser	Gly	Asp	Gln	Leu	Tyr	Arg	Met	Asn	Tyr	Met	Glu	Leu	Val	Gln
				210			215			220					
Lys	His	Val	Glu	Asp	Asp	Ala	Asp	Ile	Thr	Ile	Ser	Cys	Ala	Pro	Val
225					230				235			240			
Asp	Glu	Ser	Arg	Ala	Ser	Lys	Asn	Gly	Leu	Val	Lys	Ile	Asp	His	Thr
					245			250			255			255	
Gly	Arg	Val	Leu	Gln	Phe	Phe	Glu	Lys	Pro	Lys	Gly	Ala	Asp	Leu	Asn
				260			265			270					
Ser	Met	Arg	Val	Glu	Thr	Asn	Phe	Leu	Ser	Tyr	Ala	Ile	Asp	Asp	Ala
				275			280			285					
Gln	Lys	Tyr	Pro	Tyr	Leu	Ala	Ser	Met	Gly	Ile	Tyr	Val	Phe	Lys	Lys
				290			295			300					
Asp	Ala	Leu	Leu	Asp	Leu	Leu	Lys	Ser	Lys	Tyr	Thr	Gln	Leu	His	Asp
305					310				315			320			
Phe	Gly	Ser	Glu	Ile	Leu	Pro	Arg	Ala	Val	Leu	Asp	Tyr	Ser	Val	Gln
				325				330			335				
Ala	Cys	Ile	Phe	Thr	Gly	Tyr	Trp	Glu	Asp	Val	Gly	Thr	Ile	Lys	Ser
				340			345			350					

Phe Phe Asp Ala Asn Leu Ala Leu Thr Glu Gln Pro Ser Lys Phe Asp  
 355 360 365

Phe Tyr Asp Pro Lys Thr Pro Phe Phe Thr Ala Pro Arg Cys Leu Pro  
 370 375 380

Pro Thr Gln Leu Asp Lys Cys Lys Met Lys Tyr Ala Phe Ile Ser Asp  
 385 390 395 400

Gly Cys Leu Leu Arg Glu Cys Asn Ile Glu His Ser Val Ile Gly Val  
 405 410 415

Cys Ser Arg Val Ser Ser Gly Cys Glu Leu Lys Asp Ser Val Met Met  
 420 425 430

Gly Ala Asp Ile Tyr Glu Thr Glu Glu Glu Ala Ser Lys Leu Leu Leu  
 435 440 445

Ala Gly Lys Val Pro Val Gly Ile Gly Arg Asn Ile Lys Ile Arg Asn  
 450 455 460

Cys Ile Ile Asp Met Asn Ala Arg Ile Gly Lys Asn Val Val Ile Thr  
 465 470 475 480

Asn Ser Lys Gly Ile Gln Glu Ala Asp His Pro Glu Glu Gly Tyr Tyr  
 485 490 495

Ile Arg Ser Gly Ile Val Val Ile Leu Lys Asn Ala Thr Ile Asn Asp  
 500 505 510

Gly Ser Val Ile  
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<210> 25  
<211> 1576  
<212> DNA  
<213> Zea mays

<220>  
<221> CDS  
<222> (10)..(1563)  
<223> Shrunken-2 gene revertant form, modified to be  
heat stable

<220>  
<221> variation  
<222> (267)  
<223> k = g or t; amino acid 86 = Ala.

<220>  
<221> variation  
<222> (657)  
<223> n = a or g or c or t/u, unknown, or other.

<220>

<221> variation  
 <222> (1008)  
 <223> y = c or t.

<220>  
 <221> variation  
 <222> (1368)  
 <223> r = a or g; amino acid 453 = Pro.

<220>  
 <221> variation  
 <222> (1572)  
 <223> k = g or t.

<400> 25  
 ggaggagat atg cag ttt gca ctt gca ttg gac acg aac tca ggt cct cac 51  
 Met Gln Phe Ala Leu Ala Leu Asp Thr Asn Ser Gly Pro His  
 1 5 10

cag ata aga tct tgt gag ggt gat ggg att gac agg ttg gaa aaa tta 99  
 Gln Ile Arg Ser Cys Glu Gly Asp Gly Ile Asp Arg Leu Glu Lys Leu  
 15 20 25 30

agt att ggg ggc aga aag cag gag aaa gct ttg aga aat agg tgc ttt 147  
 Ser Ile Gly Gly Arg Lys Gln Glu Lys Ala Leu Arg Asn Arg Cys Phe  
 35 40 45

ggt ggt aga gtt gct gca act aca caa tgt att ctt acc tca gat gct 195  
 Gly Gly Arg Val Ala Ala Thr Thr Gln Cys Ile Leu Thr Ser Asp Ala  
 50 55 60

tgt cct gaa act ctt cat tct caa aca cag tcc tct agg aaa aat tat 243  
 Cys Pro Glu Thr Leu His Ser Gln Thr Gln Ser Ser Arg Lys Asn Tyr  
 65 70 75

gct gat gca aac cgt gta tct gck atc att ttg ggc gga ggc act gga 291  
 Ala Asp Ala Asn Arg Val Ser Ala Ile Ile Leu Gly Gly Thr Gly  
 80 85 90

tct cag ctc ttt cct ctg aca agc aca aga gct acg cct gct gta cct 339  
 Ser Gln Leu Phe Pro Leu Thr Ser Thr Arg Ala Thr Pro Ala Val Pro  
 95 100 105 110

gtt gga gga tgt tac agg ctt att gat atc cct atg agt aac tgc ttc 387  
 Val Gly Gly Cys Tyr Arg Leu Ile Asp Pro Met Ser Asn Cys Phe  
 115 120 125

aac agt ggt ata aat aag ata ttt gtg atg agt cag ttc aat tct act 435  
 Asn Ser Gly Ile Asn Lys Ile Phe Val Met Ser Gln Phe Asn Ser Thr  
 130 135 140

tcg ctt aac cgc cat att cat cgt aca tac ctt gaa ggc ggg atc aac 483  
 Ser Leu Asn Arg His Ile His Arg Thr Tyr Leu Glu Gly Ile Asn  
 145 150 155

ttt gct gat gga tct gta cag gta tta gcg gct aca caa atg cct gaa 531  
 Phe Ala Asp Gly Ser Val Gln Val Leu Ala Ala Thr Gln Met Pro Glu

160	165	170	
gag cca gct gga tgg ttc cag ggt aca gca gac tct atc aga aaa ttt Glu Pro Ala Gly Trp Phe Gln Gly Thr Ala Asp Ser Ile Arg Lys Phe 175 180 185 190			579
atc tgg gta ctc gag gat tat tac agt cac aaa tcc att gac aac att Ile Trp Val Leu Glu Asp Tyr Tyr Ser His Lys Ser Ile Asp Asn Ile 195 200 205			627
gta atc ttg agt ggc gat cag ctt tat ccn atg aat tac atg gaa ctt Val Ile Leu Ser Gly Asp Gln Leu Tyr Pro Met Asn Tyr Met Glu Leu 210 215 220			675
gtg cag aaa cat gtc gag gac gat gct gat atc act ata tca tgt gct Val Gln Lys His Val Glu Asp Asp Ala Asp Ile Thr Ile Ser Cys Ala 225 230 235			723
cct gtt gat gag agc cga gct tct aaa aat ggg cta gtg aag att gat Pro Val Asp Glu Ser Arg Ala Ser Lys Asn Gly Leu Val Lys Ile Asp 240 245 250			771
cat act gga cgt gta ctt caa ttc ttt gaa aaa cca aag ggt gct gat His Thr Gly Arg Val Gln Phe Phe Glu Lys Pro Lys Gly Ala Asp 255 260 265 270			819
ttg aat tct atg aga gtt gag acc aac ttc ctg agc tat gct ata gat Leu Asn Ser Met Arg Val Glu Thr Asn Phe Leu Ser Tyr Ala Ile Asp 275 280 285			867
gat gca cag aaa tat cca tac ctt gca tca atg ggc att tat gtc ttc Asp Ala Gln Lys Tyr Pro Tyr Leu Ala Ser Met Gly Ile Tyr Val Phe 290 295 300			915
aag aaa gat gca ctt tta gac ctt ctc aag tca aaa tat act caa tta Lys Lys Asp Ala Leu Leu Asp Leu Leu Lys Ser Lys Tyr Thr Gln Leu 305 310 315			963
cat gac ttt gga tct gaa atc ctc cca aga gct gta cta gat tay agt His Asp Phe Gly Ser Glu Ile Leu Pro Arg Ala Val Leu Asp Tyr Ser 320 325 330			1011
gtg cag gca tgc att ttt acg ggc tat tgg gag gat gtt gga aca atc Val Gln Ala Cys Ile Phe Thr Gly Tyr Trp Glu Asp Val Gly Thr Ile 335 340 345 350			1059
aaa tca ttc ttt gat gca aac ttg gcc ctc act gag cag cct tcc aag Lys Ser Phe Phe Asp Ala Asn Leu Ala Leu Thr Glu Gln Pro Ser Lys 355 360 365			1107
ttt gat ttt tac gat cca aaa aca cct ttc ttc act gca ccc cga tgc Phe Asp Phe Tyr Asp Pro Lys Thr Pro Phe Phe Thr Ala Pro Arg Cys 370 375 380			1155
ttg cct ccg acg caa ttg gac aag tgc aag atg aaa tat gca ttt atc Leu Pro Pro Thr Gln Leu Asp Lys Cys Lys Met Lys Tyr Ala Phe Ile 385 390 395			1203

tca gat ggt tgc tta ctg aga gaa tgc aac atc gag cat tct gtg att Ser Asp Gly Cys Leu Leu Arg Glu Cys Asn Ile Glu His Ser Val Ile	1251
400 405 410	
gga gtc tgc tca cgt gtc agc tct gga tgt gaa ctc aag gac tcc gtg Gly Val Cys Ser Arg Val Ser Ser Gly Cys Glu Leu Lys Asp Ser Val	1299
415 420 425 430	
atg atg gga gcg gac atc tat gaa act gaa gaa gct tca aag cta Met Met Gly Ala Asp Ile Tyr Glu Thr Glu Glu Ala Ser Lys Leu	1347
435 440 445	
ctg tta gct ggg aag gtc ccr gtt gga ata gga agg aac aca aag ata Leu Leu Ala Gly Lys Val Pro Val Gly Ile Gly Arg Asn Thr Lys Ile	1395
450 455 460	
agg aac tgt atc att gac atg aat gct agg att ggg aag aac gtg gtg Arg Asn Cys Ile Ile Asp Met Asn Ala Arg Ile Gly Lys Asn Val Val	1443
465 470 475	
atc aca aac agt aag ggc atc caa gag gct gat cac ccg gaa gaa ggg Ile Thr Asn Ser Lys Gly Ile Gln Glu Ala Asp His Pro Glu Glu Gly	1491
480 485 490	
tac tac ata agg tct gga atc gtg gtg atc ctg aag aat gca acc atc Tyr Tyr Ile Arg Ser Gly Ile Val Val Ile Leu Lys Asn Ala Thr Ile	1539
495 500 505 510	
aac gat ggg tct gtc ata tagatcggt gcgtktgcg Asn Asp Gly Ser Val Ile	1576
515	

<210> 26  
<211> 516  
<212> PRT  
<213> Zea mays

<400> 26

Met Gln Phe Ala Leu Ala Leu Asp Thr Asn Ser Gly Pro His Gln Ile 1 5 10 15	
Arg Ser Cys Glu Gly Asp Gly Ile Asp Arg Leu Glu Lys Leu Ser Ile 20 25 30	
Gly Gly Arg Lys Gln Glu Lys Ala Leu Arg Asn Arg Cys Phe Gly Gly 35 40 45	
Arg Val Ala Ala Thr Thr Gln Cys Ile Leu Thr Ser Asp Ala Cys Pro 50 55 60	
Glu Thr Leu His Ser Gln Thr Gln Ser Ser Arg Lys Asn Tyr Ala Asp 65 70 75 80	
Ala Asn Arg Val Ser Ala Ile Ile Leu Gly Gly Thr Gly Ser Gln	

85	90	95
Leu Phe Pro Leu Thr Ser Thr Arg Ala Thr Pro Ala Val Pro Val Gly		
100	105	110
Gly Cys Tyr Arg Leu Ile Asp Ile Pro Met Ser Asn Cys Phe Asn Ser		
115	120	125
Gly Ile Asn Lys Ile Phe Val Met Ser Gln Phe Asn Ser Thr Ser Leu		
130	135	140
Asn Arg His Ile His Arg Thr Tyr Leu Glu Gly Ile Asn Phe Ala		
145	150	155
Asp Gly Ser Val Gln Val Leu Ala Ala Thr Gln Met Pro Glu Glu Pro		
165	170	175
Ala Gly Trp Phe Gln Gly Thr Ala Asp Ser Ile Arg Lys Phe Ile Trp		
180	185	190
Val Leu Glu Asp Tyr Tyr Ser His Lys Ser Ile Asp Asn Ile Val Ile		
195	200	205
Leu Ser Gly Asp Gln Leu Tyr Pro Met Asn Tyr Met Glu Leu Val Gln		
210	215	220
Lys His Val Glu Asp Asp Ala Asp Ile Thr Ile Ser Cys Ala Pro Val		
225	230	235
Asp Glu Ser Arg Ala Ser Lys Asn Gly Leu Val Lys Ile Asp His Thr		
245	250	255
Gly Arg Val Leu Gln Phe Phe Glu Lys Pro Lys Gly Ala Asp Leu Asn		
260	265	270
Ser Met Arg Val Glu Thr Asn Phe Leu Ser Tyr Ala Ile Asp Asp Ala		
275	280	285
Gln Lys Tyr Pro Tyr Leu Ala Ser Met Gly Ile Tyr Val Phe Lys Lys		
290	295	300
Asp Ala Leu Leu Asp Leu Leu Lys Ser Lys Tyr Thr Gln Leu His Asp		
305	310	320
Phe Gly Ser Glu Ile Leu Pro Arg Ala Val Leu Asp Tyr Ser Val Gln		
325	330	335
Ala Cys Ile Phe Thr Gly Tyr Trp Glu Asp Val Gly Thr Ile Lys Ser		
340	345	350
Phe Phe Asp Ala Asn Leu Ala Leu Thr Glu Gln Pro Ser Lys Phe Asp		
355	360	365
Phe Tyr Asp Pro Lys Thr Pro Phe Phe Thr Ala Pro Arg Cys Leu Pro		
370	375	380
Pro Thr Gln Leu Asp Lys Cys Lys Met Lys Tyr Ala Phe Ile Ser Asp		

385	390	395	400
Gly Cys Leu Leu Arg Glu Cys Asn Ile Glu His Ser Val Ile Gly Val			
405	410	415	
Cys Ser Arg Val Ser Ser Gly Cys Glu Leu Lys Asp Ser Val Met Met			
420	425	430	
Gly Ala Asp Ile Tyr Glu Thr Glu Glu Ala Ser Lys Leu Leu Leu			
435	440	445	
Ala Gly Lys Val Pro Val Gly Ile Gly Arg Asn Thr Lys Ile Arg Asn			
450	455	460	
Cys Ile Ile Asp Met Asn Ala Arg Ile Gly Lys Asn Val Val Ile Thr			
465	470	475	480
Asn Ser Lys Gly Ile Gln Glu Ala Asp His Pro Glu Glu Gly Tyr Tyr			
485	490	495	
Ile Arg Ser Gly Ile Val Val Ile Leu Lys Asn Ala Thr Ile Asn Asp			
500	505	510	
Gly Ser Val Ile			
515			

<210> 27  
<211> 1576  
<212> DNA  
<213> Zea mays

<220>  
<221> CDS  
<222> (10)..(1563)  
<223> Shrunken-2 gene revertant form, modified to be  
heat stable

<220>  
<221> variation  
<222> (267)  
<223> k = g or t; amino acid 86 = Ala.

<220>  
<221> variation  
<222> (540)  
<223> n = a or g or c or t/u, unknown, or other.

<220>  
<221> variation  
<222> {1008)  
<223> y = c or t.

<220>  
<221> variation  
<222> (1287)  
<223> y = c or t.

<220>  
<221> variation

<222> (1368)  
<223> r = a or g; amino acid 453 = Pro.

<220>  
<221> variation  
<222> (1572)  
<223> k = g or t.

<400> 27  
ggaggagat atg cag ttt gca ctt gca ttg gac acg aac tca ggt cct cac 51  
Met Gln Phe Ala Leu Ala Leu Asp Thr Asn Ser Gly Pro His  
1 5 10

cag ata aga tct tgt gag ggt gat ggg att gac agg ttg gaa aaa tta 99  
Gln Ile Arg Ser Cys Glu Gly Asp Gly Ile Asp Arg Leu Glu Lys Leu  
15 20 25 30

agt att ggg ggc aga aag cag gag aaa gct ttg aga aat agg tgc ttt 147  
Ser Ile Gly Gly Arg Lys Gln Glu Lys Ala Leu Arg Asn Arg Cys Phe  
35 40 45

ggt ggt aga gtt gct gca act aca caa tgt att ctt acc tca gat gct 195  
Gly Gly Arg Val Ala Ala Thr Thr Gln Cys Ile Leu Thr Ser Asp Ala  
50 55 60

tgt cct gaa act ctt cat tct caa aca cag tcc tct agg aaa aat tat 243  
Cys Pro Glu Thr Leu His Ser Gln Thr Gln Ser Ser Arg Lys Asn Tyr  
65 70 75

gct gat gca aac cgt gta tct gck atc att ttg ggc gga ggc act gga 291  
Ala Asp Ala Asn Arg Val Ser Ala Ile Ile Leu Gly Gly Thr Gly  
80 85 90

tct cag ctc ttt cct ctg aca agc aca aga gct acg cct gct gta cct 339  
Ser Gln Leu Phe Pro Leu Thr Ser Thr Arg Ala Thr Pro Ala Val Pro  
95 100 105 110

gtt gga gga tgt tac agg ctt att gat atc cct atg agt aac tgc ttc 387  
Val Gly Cys Tyr Arg Leu Ile Asp Ile Pro Met Ser Asn Cys Phe  
115 120 125

aac agt ggt ata aat aag ata ttt gtg atg agt cag ttc aat tct act 435  
Asn Ser Gly Ile Asn Lys Ile Phe Val Met Ser Gln Phe Asn Ser Thr  
130 135 140

tcg ctt aac cgc cat att cat cgt aca tac ctt gaa ggc ggg atc aac 483  
Ser Leu Asn Arg His Ile His Arg Thr Tyr Leu Glu Gly Ile Asn  
145 150 155

ttt gct gat gga tct gta cag gta tta gcg gct aca caa atg cct gaa 531  
Phe Ala Asp Gly Ser Val Gln Val Leu Ala Ala Thr Gln Met Pro Glu  
160 165 170

gag cca gtn gga tgg ttc cag ggt aca gca gac tct atc aga aaa ttt Glu Pro Val Gly Trp Phe Gln Gly Thr Ala Asp Ser Ile Arg Lys Phe 175 180 185 190	579
atc tgg gta ctc gag gat tat tac agt cac aaa tcc att gac aac att Ile Trp Val Leu Glu Asp Tyr Tyr Ser His Lys Ser Ile Asp Asn Ile 195 200 205	627
gta atc ttg agt ggc gat cag ctt tat cgg atg aat tac atg gaa ctt Val Ile Ieu Ser Gly Asp Gln Leu Tyr Arg Met Asn Tyr Met Glu Leu 210 215 220	675
gtg cag aaa cat gtc gag gac gat gct gat atc act ata tca tgt gct Val Gln Lys His Val Glu Asp Asp Ala Asp Ile Thr Ile Ser Cys Ala 225 230 235	723
cct gtt gat gag agc cga gct tct aaa aat ggg cta gtg aag att gat Pro Val Asp Glu Ser Arg Ala Ser Lys Asn Gly Leu Val Lys Ile Asp 240 245 250	771
cat act gga cgt gta ctt caa ttc ttt gaa aaa cca aag ggt gct gat His Thr Gly Arg Val Leu Gln Phe Phe Glu Lys Pro Lys Gly Ala Asp 255 260 265 270	819
ttg aat tct atg aga gtt gag acc aac ttc ctg agc tat gct ata gat Leu Asn Ser Met Arg Val Glu Thr Asn Phe Leu Ser Tyr Ala Ile Asp 275 280 285	867
gat gca cag aaa tat cca tac ctt gca tca atg ggc att tat gtc ttc Asp Ala Gln Lys Tyr Pro Tyr Leu Ala Ser Met Gly Ile Tyr Val Phe 290 295 300	915
aag aaa gat gca ctt tta gac ctt ctc aag tca aaa tat act caa tta Lys Lys Asp Ala Leu Leu Asp Leu Leu Lys Ser Lys Tyr Thr Gln Leu 305 310 315	963
cat gac ttt gga tct gaa atc ctc cca aga gct gta cta gat cay agt His Asp Phe Gly Ser Glu Ile Leu Pro Arg Ala Val Leu Asp His Ser 320 325 330	1011
gtg cag gca tgc att ttt acg ggc tat tgg gag gat gtt gga aca atc Val Gln Ala Cys Ile Phe Thr Gly Tyr Trp Glu Asp Val Gly Thr Ile 335 340 345 350	1059
aaa tca ttc ttt gat gca aac ttg gcc ctc act gag cag cct tcc aag Lys Ser Phe Asp Ala Asn Leu Ala Leu Thr Glu Gln Pro Ser Lys 355 360 365	1107
tta gat ttt tac gat cca aaa aca cct ttc ttc act gca ccc cga tgc Phe Asp Phe Tyr Asp Pro Lys Thr Pro Phe Phe Thr Ala Pro Arg Cys 370 375 380	1155
ttg cct ccg acg caa ttg gac aag tgc aag atg aaa tat gca ttt atc Leu Pro Pro Thr Gln Leu Asp Lys Cys Lys Met Lys Tyr Ala Phe Ile 385 390 395	1203
tca gat ggt tgc tta ctg aga gaa tgc aac atc gag cat tct gtg att	1251

Ser Asp Gly Cys Leu Leu Arg Glu Cys Asn Ile Glu His Ser Val Ile  
 400 405 410

gga gtc tgc tca cgt gtc agc tct gga tgt gaa tty aag gac tcc gtg 1299  
 Gly Val Cys Ser Arg Val Ser Ser Gly Cys Glu Phe Lys Asp Ser Val  
 415 420 425 430

atg atg gga gcg gac atc tat gaa act gaa gaa gct tca aag cta 1347  
 Met Met Gly Ala Asp Ile Tyr Glu Thr Glu Glu Ala Ser Lys Leu  
 435 440 445

ctg tta gct ggg aag gtc ccr gtt gga ata gga agg aac aca aag ata 1395  
 Leu Leu Ala Gly Lys Val Pro Val Gly Ile Gly Arg Asn Thr Lys Ile  
 450 455 460

agg aac tgt atc att gac atg aat gct agg att ggg aag aac gtg gtg 1443  
 Arg Asn Cys Ile Ile Asp Met Asn Ala Arg Ile Gly Lys Asn Val Val  
 465 470 475

atc aca aac agt aag ggc atc caa gag gct gat cac ccg gaa gaa ggg 1491  
 Ile Thr Asn Ser Lys Gly Ile Gln Glu Ala Asp His Pro Glu Glu Gly  
 480 485 490

tac tac ata agg tct gga atc gtg gtg atc ctg aag aat gca acc atc 1539  
 Tyr Tyr Ile Arg Ser Gly Ile Val Val Ile Leu Lys Asn Ala Thr Ile  
 495 500 505 510

aac gat ggg tct gtc ata tagatccggct gcgtktgcg 1576  
 Asn Asp Gly Ser Val Ile  
 515

<210> 28  
 <211> 516  
 <212> PRT  
 <213> Zea mays

<400> 28

Met Gln Phe Ala Leu Ala Leu Asp Thr Asn Ser Gly Pro His Gln Ile  
 1 5 10 15

Arg Ser Cys Glu Gly Asp Gly Ile Asp Arg Leu Glu Lys Leu Ser Ile  
 20 25 30

Gly Gly Arg Lys Gln Glu Lys Ala Leu Arg Asn Arg Cys Phe Gly Gly  
 35 40 45

Arg Val Ala Ala Thr Thr Gln Cys Ile Leu Thr Ser Asp Ala Cys Pro  
 50 55 60

Glu Thr Leu His Ser Gln Thr Gln Ser Ser Arg Lys Asn Tyr Ala Asp  
 65 70 75 80

Ala Asn Arg Val Ser Ala Ile Ile Leu Gly Gly Gly Thr Gly Ser Gln  
 85 90 95

Leu Phe Pro Leu Thr Ser Thr Arg Ala Thr Pro Ala Val Pro Val Gly  
 100 105 110  
 Gly Cys Tyr Arg Leu Ile Asp Ile Pro Met Ser Asn Cys Phe Asn Ser  
 115 120 125  
 Gly Ile Asn Lys Ile Phe Val Met Ser Gln Phe Asn Ser Thr Ser Leu  
 130 135 140  
 Asn Arg His Ile His Arg Thr Tyr Leu Glu Gly Gly Ile Asn Phe Ala  
 145 150 155 160  
 Asp Gly Ser Val Gln Val Leu Ala Ala Thr Gln Met Pro Glu Glu Pro  
 165 170 175  
 Val Gly Trp Phe Gln Gly Thr Ala Asp Ser Ile Arg Lys Phe Ile Trp  
 180 185 190  
 Val Leu Glu Asp Tyr Tyr Ser His Lys Ser Ile Asp Asn Ile Val Ile  
 195 200 205  
 Leu Ser Gly Asp Gln Leu Tyr Arg Met Asn Tyr Met Glu Leu Val Gln  
 210 215 220  
 Lys His Val Glu Asp Asp Ala Asp Ile Thr Ile Ser Cys Ala Pro Val  
 225 230 235 240  
 Asp Glu Ser Arg Ala Ser Lys Asn Gly Leu Val Lys Ile Asp His Thr  
 245 250 255  
 Gly Arg Val Leu Gln Phe Phe Glu Lys Pro Lys Gly Ala Asp Leu Asn  
 260 265 270  
 Ser Met Arg Val Glu Thr Asn Phe Leu Ser Tyr Ala Ile Asp Asp Ala  
 275 280 285  
 Gln Lys Tyr Pro Tyr Leu Ala Ser Met Gly Ile Tyr Val Phe Lys Lys  
 290 295 300  
 Asp Ala Leu Leu Asp Leu Leu Lys Ser Lys Tyr Thr Gln Leu His Asp  
 305 310 315 320  
 Phe Gly Ser Glu Ile Leu Pro Arg Ala Val Leu Asp His Ser Val Gln  
 325 330 335  
 Ala Cys Ile Phe Thr Gly Tyr Trp Glu Asp Val Gly Thr Ile Lys Ser  
 340 345 350  
 Phe Phe Asp Ala Asn Leu Ala Leu Thr Glu Gln Pro Ser Lys Phe Asp  
 355 360 365  
 Phe Tyr Asp Pro Lys Thr Pro Phe Phe Thr Ala Pro Arg Cys Leu Pro  
 370 375 380  
 Pro Thr Gln Leu Asp Lys Cys Lys Met Lys Tyr Ala Phe Ile Ser Asp  
 385 390 395 400

Gly Cys Leu Leu Arg Glu Cys Asn Ile Glu His Ser Val Ile Gly Val  
405 410 415

Cys Ser Arg Val Ser Ser Gly Cys Glu Phe Lys Asp Ser Val Met Met  
420 425 430

Gly Ala Asp Ile Tyr Glu Thr Glu Glu Ala Ser Lys Leu Leu Leu  
435 440 445

Ala Gly Lys Val Pro Val Gly Ile Gly Arg Asn Thr Lys Ile Arg Asn  
450 455 460

Cys Ile Ile Asp Met Asn Ala Arg Ile Gly Lys Asn Val Val Ile Thr  
465 470 475 480

Asn Ser Lys Gly Ile Gln Glu Ala Asp His Pro Glu Glu Gly Tyr Tyr  
485 490 495

Ile Arg Ser Gly Ile Val Val Ile Leu Lys Asn Ala Thr Ile Asn Asp  
500 505 510

Gly Ser Val Ile  
515

<210> 29  
<211> 1576  
<212> DNA  
<213> Zea mays

<220>  
<221> CDS  
<222> (10)...(1563)  
<223> Shrunken-2 gene revertant form, modified to be  
heat stable

<220>  
<221> variation  
<222> (267)  
<223> k = g or t; amino acid 86 = Ala.

<220>  
<221> variation  
<222> (981)  
<223> r = g or a.

<220>  
<221> variation  
<222> (1008)  
<223> y = c or t.

<220>  
<221> variation  
<222> (1086)  
<223> n = a or g or c or t/u, unknown, or other.

<220>

<221> variation  
 <222> (1197)  
 <223> n = a or g or c or t/u, unknown, or other.

<220>  
 <221> variation  
 <222> (1368)  
 <223> r = a or g; amino acid 453 = Pro.

<220>  
 <221> variation  
 <222> (1572)  
 <223> k = g or t.

<400> 29  
 ggaggagat atg cag ttt gca ctt gca ttg gac acg aac tca ggt cct cac 51  
 Met Gln Phe Ala Leu Ala Leu Asp Thr Asn Ser Gly Pro His  
 1 5 10

cag ata aga tct tgt gag ggt gat ggg att gac agg ttg gaa aaa tta 99  
 Gln Ile Arg Ser Cys Glu Gly Asp Gly Ile Asp Arg Leu Glu Lys Leu  
 15 20 25 30

agt att ggg ggc aga aag cag gag aaa gct ttg aga aat agg tgc ttt 147  
 Ser Ile Gly Gly Arg Lys Gln Glu Lys Ala Leu Arg Asn Arg Cys Phe  
 35 40 45

ggt ggt aga gtt gct gca act aca caa tgt att ctt acc tca gat gct 195  
 Gly Gly Arg Val Ala Ala Thr Thr Gln Cys Ile Leu Thr Ser Asp Ala  
 50 55 60

tgt cct gaa act ctt cat tct caa aca cag tcc tct agg aaa aat tat 243  
 Cys Pro Glu Thr Leu His Ser Gln Thr Gln Ser Ser Arg Lys Asn Tyr  
 65 70 75

gct gat gca aac cgt gta tct gck atc att ttg ggc gga ggc act gga 291  
 Ala Asp Ala Asn Arg Val Ser Ala Ile Ile Leu Gly Gly Gly Thr Gly  
 80 85 90

tct cag ctc ttt cct ctg aca agc aca aga gct acg cct gct gta cct 339  
 Ser Gln Leu Phe Pro Leu Thr Ser Thr Arg Ala Thr Pro Ala Val Pro  
 95 100 105 110

gtt gga gga tgt tac agg ctt att gat atc cct atg agt aac tgc ttc 387  
 Val Gly Gly Cys Tyr Arg Leu Ile Asp Ile Pro Met Ser Asn Cys Phe  
 115 120 125

aac agt ggt ata aat aag ata ttt gtg atg agt cag ttc aat tct act 435  
 Asn Ser Gly Ile Asn Lys Ile Phe Val Met Ser Gln Phe Asn Ser Thr  
 130 135 140

tcg ctt aac cgc cat att cat cgt aca tac ctt gaa ggc ggg atc aac 483  
 Ser Leu Asn Arg His Ile His Arg Thr Tyr Leu Glu Gly Gly Ile Asn  
 145 150 155

ttt gct gat gga tct gta cag gta tta gcg gct aca caa atg cct gaa 531  
 Phe Ala Asp Gly Ser Val Gln Val Leu Ala Ala Thr Gln Met Pro Glu

160	165	170	
gag cca gct gga tgg ttc cag ggt aca gca gac tct atc aga aaa ttt Glu Pro Ala Gly Trp Phe Gln Gly Thr Ala Asp Ser Ile Arg Lys Phe 175 180 185 190			579
atc tgg gta ctc gag gat tat tac agt cac aaa tcc att gac aac att Ile Trp Val Leu Glu Asp Tyr Tyr Ser His Lys Ser Ile Asp Asn Ile 195 200 205			627
gta atc ttg agt ggc gat cag ctt tat cgg atg aat tac atg gaa ctt Val Ile Leu Ser Gly Asp Gln Leu Tyr Arg Met Asn Tyr Met Glu Leu 210 215 220			675
gtg cag aaa cat gtc gag gac gat gct gat atc act ata tca tgt gct Val Gln Lys His Val Glu Asp Asp Ala Asp Ile Thr Ile Ser Cys Ala 225 230 235			723
cct gtt gat gag agc cga gct tct aaa aat ggg cta gtg aag att gat Pro Val Asp Glu Ser Arg Ala Ser Lys Asn Gly Leu Val Lys Ile Asp 240 245 250			771
cat act gga cgt gta ctt caa ttc ttt gaa aaa cca aag ggt gct gat His Thr Gly Arg Val Gln Phe Phe Glu Lys Pro Lys Gly Ala Asp 255 260 265 270			819
ttg aat tct atg aga gtt gag acc aac ttc ctg agc tat gct ata gat Leu Asn Ser Met Arg Val Glu Thr Asn Phe Leu Ser Tyr Ala Ile Asp 275 280 285			867
gat gca cag aaa tat cca tac ctt gca tca atg ggc att tat gtc ttc Asp Ala Gln Lys Tyr Pro Tyr Leu Ala Ser Met Gly Ile Tyr Val Phe 290 295 300			915
aag aaa gat gca ctt tta gac ctt ctc aag tca aaa tat act caa tta Lys Lys Asp Ala Leu Leu Asp Leu Lys Ser Lys Tyr Thr Gln Leu 305 310 315			963
cat gac ttt gga tct aar atc ctc cca aga gct gta cta gat cay agt His Asp Phe Gly Ser Lys Ile Leu Pro Arg Ala Val Leu Asp His Ser 320 325 330			1011
gtg cag gca tgc att ttt acg ggc tat tgg gag gat gtt gga aca atc Val Gln Ala Cys Ile Phe Thr Gly Tyr Trp Glu Asp Val Gly Thr Ile 335 340 345 350			1059
aaa tca ttc ttt gat gca aac ttg gtn ctc act gag cag cct tcc aag Lys Ser Phe Phe Asp Ala Asn Leu Val Thr Glu Gln Pro Ser Lys 355 360 365			1107
ttt gat ttt tac gat cca aaa aca cct ttc ttc act gca ccc cga tgc Phe Asp Phe Tyr Asp Pro Lys Thr Pro Phe Phe Thr Ala Pro Arg Cys 370 375 380			1155
ttg cct ccg acg caa ttg gac aag tgc aag atg aaa tat gtn ttt atc Leu Pro Pro Thr Gln Leu Asp Lys Cys Lys Met Lys Tyr Val Phe Ile 385 390 395			1203

tca gat ggt tgc tta ctg aga gaa tgc aac atc gag cat tct gtg att 1251  
 Ser Asp Gly Cys Leu Leu Arg Glu Cys Asn Ile Glu His Ser Val Ile  
 400 405 410

gga gtc tgc tca cgt gtc agc tct gga tgt gaa ctc aag gac tcc gtg 1299  
 Gly Val Cys Ser Arg Val Ser Ser Gly Cys Glu Leu Lys Asp Ser Val  
 415 420 425 430

atg atg gga gcg gac atc tat gaa act gaa gaa gac tca aag cta 1347  
 Met Met Gly Ala Asp Ile Tyr Glu Thr Glu Glu Ala Ser Lys Leu  
 435 440 445

ctg tta gct ggg aag gtc ccr gtt gga ata gga agg aac aca aag ata 1395  
 Leu Leu Ala Gly Lys Val Pro Val Gly Ile Gly Arg Asn Thr Lys Ile  
 450 455 460

agg aac tgt atc att gag atg aat gct agg att ggg aag aac gtg gtg 1443  
 Arg Asn Cys Ile Ile Asp Met Asn Ala Arg Ile Gly Lys Asn Val Val  
 465 470 475

atc aca aac agt aag ggc atc caa gag gct gat cac ccg gaa gaa ggg 1491  
 Ile Thr Asn Ser Lys Gly Ile Gln Glu Ala Asp His Pro Glu Glu Gly  
 480 485 490

tac tac ata agg tct gga atc gtg gtg atc ctg aag aat gca acc atc 1539  
 Tyr Tyr Ile Arg Ser Gly Ile Val Val Ile Leu Lys Asn Ala Thr Ile  
 495 500 505 510

aac gat ggg tct gtc ata tagatcggt gcgtktgcg 1576  
 Asn Asp Gly Ser Val Ile  
 515

<210> 30  
 <211> 516  
 <212> PRT  
 <213> Zea mays

<400> 30

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Arg Ser Cys Glu Gly Asp Gly Ile Asp Arg Leu Glu Lys Leu Ser Ile  
 20 25 30

Gly Gly Arg Lys Gln Glu Lys Ala Leu Arg Asn Arg Cys Phe Gly Gly  
 35 40 45

Arg Val Ala Ala Thr Thr Gln Cys Ile Leu Thr Ser Asp Ala Cys Pro  
 50 55 60

Glu Thr Leu His Ser Gln Thr Gln Ser Ser Arg Lys Asn Tyr Ala Asp  
 65 70 75 80

Ala Asn Arg Val Ser Ala Ile Ile Leu Gly Gly Thr Gly Ser Gln

85

90

95

Leu Phe Pro Leu Thr Ser Thr Arg Ala Thr Pro Ala Val Pro Val Gly  
 100 105 110

Gly Cys Tyr Arg Leu Ile Asp Ile Pro Met Ser Asn Cys Phe Asn Ser  
 115 120 125

Gly Ile Asn Lys Ile Phe Val Met Ser Gln Phe Asn Ser Thr Ser Leu  
 130 135 140

Asn Arg His Ile His Arg Thr Tyr Leu Glu Gly Ile Asn Phe Ala  
 145 150 155 160

Asp Gly Ser Val Gln Val Leu Ala Ala Thr Gln Met Pro Glu Glu Pro  
 165 170 175

Ala Gly Trp Phe Gln Gly Thr Ala Asp Ser Ile Arg Lys Phe Ile Trp  
 180 185 190

Val Leu Glu Asp Tyr Tyr Ser His Lys Ser Ile Asp Asn Ile Val Ile  
 195 200 205

Leu Ser Gly Asp Gln Leu Tyr Arg Met Asn Tyr Met Glu Leu Val Gln  
 210 215 220

Lys His Val Glu Asp Asp Ala Asp Ile Thr Ile Ser Cys Ala Pro Val  
 225 230 235 240

Asp Glu Ser Arg Ala Ser Lys Asn Gly Leu Val Lys Ile Asp His Thr  
 245 250 255

Gly Arg Val Leu Gln Phe Phe Glu Lys Pro Lys Gly Ala Asp Leu Asn  
 260 265 270

Ser Met Arg Val Glu Thr Asn Phe Leu Ser Tyr Ala Ile Asp Asp Ala  
 275 280 285

Gln Lys Tyr Pro Tyr Leu Ala Ser Met Gly Ile Tyr Val Phe Lys Lys  
 290 295 300

Asp Ala Leu Leu Asp Leu Leu Lys Ser Lys Tyr Thr Gln Leu His Asp  
 305 310 315 320

Phe Gly Ser Lys Ile Leu Pro Arg Ala Val Leu Asp His Ser Val Gln  
 325 330 335

Ala Cys Ile Phe Thr Gly Tyr Trp Glu Asp Val Gly Thr Ile Lys Ser  
 340 345 350

Phe Phe Asp Ala Asn Leu Val Leu Thr Glu Gln Pro Ser Lys Phe Asp  
 355 360 365

Phe Tyr Asp Pro Lys Thr Pro Phe Phe Thr Ala Pro Arg Cys Leu Pro  
 370 375 380

Pro Thr Gln Leu Asp Lys Cys Lys Met Lys Tyr Val Phe Ile Ser Asp

385	390	395	400
Gly Cys Leu Leu Arg Glu Cys Asn Ile Glu His Ser Val Ile Gly Val			
405	410	415	
Cys Ser Arg Val Ser Ser Gly Cys Glu Leu Lys Asp Ser Val Met Met			
420	425	430	
Gly Ala Asp Ile Tyr Glu Thr Glu Glu Ala Ser Lys Leu Leu Leu			
435	440	445	
Ala Gly Lys Val Pro Val Gly Ile Gly Arg Asn Thr Lys Ile Arg Asn			
450	455	460	
Cys Ile Ile Asp Met Asn Ala Arg Ile Gly Lys Asn Val Val Ile Thr			
465	470	475	480
Asn Ser Lys Gly Ile Gln Glu Ala Asp His Pro Glu Glu Gly Tyr Tyr			
485	490	495	
Ile Arg Ser Gly Ile Val Val Ile Leu Lys Asn Ala Thr Ile Asn Asp			
500	505	510	
Gly Ser Val Ile			
515			

<210> 31  
<211> 1576  
<212> DNA  
<213> Zea mays

<220>  
<221> CDS  
<222> (10)..(1563)  
<223> Shrunken-2 gene revertant form, modified to be  
heat stable

<220>  
<221> variation  
<222> (267)  
<223> k = g or t; amino acid 86 = Ala.

<220>  
<221> variation  
<222> (1008)  
<223> y = c or t.

<220>  
<221> variation  
<222> (1368)  
<223> r = a or g; amino acid 453 = Pro.

<220>  
<221> variation  
<222> (1572)  
<223> k = g or t.

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 ggaggagat atg cag ttt gca ctt gca ttg gac acg aac tca ggt cct cac 51  
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 1 5 10

cag ata aga tct tgt gag ggt gat ggg att gac agg ttg gaa aaa tta 99  
 Gln Ile Arg Ser Cys Glu Gly Asp Gly Ile Asp Arg Leu Glu Lys Leu  
 15 20 25 30

agt att ggg ggc aga aag cag gag aaa gct ttg aga aat agg tgc ttt 147  
 Ser Ile Gly Gly Arg Lys Gln Glu Lys Ala Leu Arg Asn Arg Cys Phe  
 35 40 45

ggg ggt aga gtt gct gca act aca caa tgt att ctt acc tca gat gct 195  
 Gly Gly Arg Val Ala Ala Thr Thr Gln Cys Ile Leu Thr Ser Asp Ala  
 50 55 60

tgt cct gaa act ctt cat tct caa aca cag tcc tct agg aaa aat tat 243  
 Cys Pro Glu Thr Leu His Ser Gln Thr Gln Ser Ser Arg Lys Asn Tyr  
 65 70 75

gct gat gca aac cgt gta tct gck atc att ttg ggc gga ggc act gga 291  
 Ala Asp Ala Asn Arg Val Ser Ala Ile Ile Leu Gly Gly Thr Gly  
 80 85 90

tct cag ctc ttt cct ctg aca agc aca aga gct acg cct gct gta cct 339  
 Ser Gln Leu Phe Pro Leu Thr Ser Thr Arg Ala Thr Pro Ala Val Pro  
 95 100 105 110

gtt gga gga tgt tac agg ctt att gat atc cct atg agt aac tgc ttc 387  
 Val Gly Gly Cys Tyr Arg Leu Ile Asp Ile Pro Met Ser Asn Cys Phe  
 115 120 125

aac agt ggt ata aat aag ata ttt gtg atg agt cag ttc aat tct act 435  
 Asn Ser Gly Ile Asn Lys Ile Phe Val Met Ser Gln Phe Asn Ser Thr  
 130 135 140

tgc ctt aac cgc cat att cat cgt aca tac ctt gaa ggc ggg atc aac 483  
 Ser Leu Asn Arg His Ile His Arg Thr Tyr Leu Glu Gly Gly Ile Asn  
 145 150 155

ttt gct gat gga tct gta cag gta tta gcg gct aca caa atg cct gaa 531  
 Phe Ala Asp Gly Ser Val Gln Val Leu Ala Ala Thr Gln Met Pro Glu  
 160 165 170

gag cca gct gga tgg ttc cag ggt aca gca gac tct atc aga aaa ttt 579  
 Glu Pro Ala Gly Trp Phe Gln Gly Thr Ala Asp Ser Ile Arg Lys Phe  
 175 180 185 190

atc tgg gta ctc gag gat tat tac agt cac aaa tcc att gac aac att 627  
 Ile Trp Val Leu Glu Asp Tyr Tyr Ser His Lys Ser Ile Asp Asn Ile  
 195 200 205

gta atc ttg agt ggc gat cag ctt tat cgg atg aat tac atg gaa ctt 675  
 Val Ile Leu Ser Gly Asp Gln Leu Tyr Arg Met Asn Tyr Met Glu Leu  
 210 215 220

gtg cag aaa cat gtc gag gac gat gct gat atc act ata tca tgt gct Val Gln Lys His Val Glu Asp Asp Ala Asp Ile Thr Ile Ser Cys Ala 225 230 235	723
cct gtt gat gag agc cga gct tct aaa aat ggg cta gtg aag att gat Pro Val Asp Glu Ser Arg Ala Ser Lys Asn Gly Leu Val Lys Ile Asp 240 245 250	771
cat act gga cgt gta ctt caa ttc ttt gaa aaa cca aag ggt gct gat His Thr Gly Arg Val Leu Gln Phe Phe Glu Lys Pro Lys Gly Ala Asp 255 260 265 270	819
ttg aat tct atg aga gtt gag acc aac ttc ctg agc tat gct ata gat Leu Asn Ser Met Arg Val Glu Thr Asn Phe Leu Ser Tyr Ala Ile Asp 275 280 285	867
gat gca cag aaa tat cca tac ctt gca tca atg ggc att tat gtc ttc Asp Ala Gln Lys Tyr Pro Tyr Leu Ala Ser Met Gly Ile Tyr Val Phe 290 295 300	915
aag aaa gat gca ctt tta gac ctt ctc aag tca aaa tat act caa tta Lys Lys Asp Ala Leu Leu Asp Leu Leu Lys Ser Lys Tyr Thr Gln Leu 305 310 315	963
cat gac ttt gga tct gaa atc ctc cca aga gct gta cta gat tty agt His Asp Phe Gly Ser Glu Ile Leu Pro Arg Ala Val Leu Asp Phe Ser 320 325 330	1011
gtg cag gca tgc att ttt acg ggc tat tgg gag gat gtt gga aca atc Val Gln Ala Cys Ile Phe Thr Gly Tyr Trp Glu Asp Val Gly Thr Ile 335 340 345 350	1059
aaa tca ttc ttt gat gca aac ttg gcc ctc act gag cag cct tcc aag Lys Ser Phe Asp Ala Asn Leu Ala Leu Thr Glu Gln Pro Ser Lys 355 360 365	1107
ttt gat ttt tac gat cca aaa aca cct ttc ttc act gca ccc cga tgc Phe Asp Phe Tyr Asp Pro Lys Thr Pro Phe Thr Ala Pro Arg Cys 370 375 380	1155
ttg cct ccg acg caa ttg gac aag tgc aag atg aaa tat gca ttt atc Leu Pro Pro Thr Gln Leu Asp Lys Cys Lys Met Lys Tyr Ala Phe Ile 385 390 395	1203
tca gat ggt tgc tta ctg aga gaa tgc aac atc gag cat tct gtg att Ser Asp Gly Cys Leu Leu Arg Glu Cys Asn Ile Glu His Ser Val Ile 400 405 410	1251
gga gtc tgc tca cgt gtc agc tct gga tgt gaa ctc aag gac tcc gtg Gly Val Cys Ser Arg Val Ser Ser Gly Cys Glu Leu Lys Asp Ser Val 415 420 425 430	1299
atg atg gga gcg gac atc tat gaa act gaa gaa gaa gct tca aag cta Met Met Gly Ala Asp Ile Tyr Glu Thr Glu Glu Ala Ser Lys Leu 435 440 445	1347

ctg tta gct ggg aag gtc ccr gtt gga ata gga agg aac aca aag ata 1395  
 Leu Leu Ala Gly Lys Val Pro Val Gly Ile Gly Arg Asn Thr Lys Ile  
 450 455 460

agg aac tgt atc att gac atg aat gct agg att ggg aag aac gtg gtg 1443  
 Arg Asn Cys Ile Ile Asp Met Asn Ala Arg Ile Gly Lys Asn Val Val  
 465 470 475

atc aca aac agt aag ggc atc caa gag gct gat cac ccg gaa gaa ggg 1491  
 Ile Thr Asn Ser Lys Gly Ile Gln Glu Ala Asp His Pro Glu Glu Gly  
 480 485 490

tac tac ata agg tct gga atc gtg gtg atc ctg aag aat gca acc atc 1539  
 Tyr Tyr Ile Arg Ser Gly Ile Val Val Ile Leu Lys Asn Ala Thr Ile  
 495 500 505 510

aac gat ggg tct gtc ata tagatcggt gcgtktgcg 1576  
 Asn Asp Gly Ser Val Ile  
 515

<210> 32  
<211> 516  
<212> PRT  
<213> Zea mays

<400> 32

Met Gln Phe Ala Leu Ala Leu Asp Thr Asn Ser Gly Pro His Gln Ile  
 1 5 10 15

Arg Ser Cys Glu Gly Asp Gly Ile Asp Arg Leu Glu Lys Leu Ser Ile  
 20 25 30

Gly Gly Arg Lys Gln Glu Lys Ala Leu Arg Asn Arg Cys Phe Gly Gly  
 35 40 45

Arg Val Ala Ala Thr Thr Gln Cys Ile Leu Thr Ser Asp Ala Cys Pro  
 50 55 60

Glu Thr Leu His Ser Gln Thr Gln Ser Ser Arg Lys Asn Tyr Ala Asp  
 65 70 75 80

Ala Asn Arg Val Ser Ala Ile Ile Leu Gly Gly Thr Gly Ser Gln  
 85 90 95

Leu Phe Pro Leu Thr Ser Thr Arg Ala Thr Pro Ala Val Pro Val Gly  
 100 105 110

Gly Cys Tyr Arg Leu Ile Asp Ile Pro Met Ser Asn Cys Phe Asn Ser  
 115 120 125

Gly Ile Asn Lys Ile Phe Val Met Ser Gln Phe Asn Ser Thr Ser Leu  
 130 135 140

Asn Arg His Ile His Arg Thr Tyr Leu Glu Gly Gly Ile Asn Phe Ala  
 145 150 155 160

Asp Gly Ser Val Gln Val Leu Ala Ala Thr Gln Met Pro Glu Glu Pro  
                   165                  170                  175  
 Ala Gly Trp Phe Gln Gly Thr Ala Asp Ser Ile Arg Lys Phe Ile Trp  
                   180                  185                  190  
 Val Leu Glu Asp Tyr Tyr Ser His Lys Ser Ile Asp Asn Ile Val Ile  
                   195                  200                  205  
 Leu Ser Gly Asp Gln Leu Tyr Arg Met Asn Tyr Met Glu Leu Val Gln  
                   210                  215                  220  
 Lys His Val Glu Asp Asp Ala Asp Ile Thr Ile Ser Cys Ala Pro Val  
                   225                  230                  235                  240  
 Asp Glu Ser Arg Ala Ser Lys Asn Gly Leu Val Lys Ile Asp His Thr  
                   245                  250                  255  
 Gly Arg Val Leu Gln Phe Phe Glu Lys Pro Lys Gly Ala Asp Leu Asn  
                   260                  265                  270  
 Ser Met Arg Val Glu Thr Asn Phe Leu Ser Tyr Ala Ile Asp Asp Ala  
                   275                  280                  285  
 Gln Lys Tyr Pro Tyr Leu Ala Ser Met Gly Ile Tyr Val Phe Lys Lys  
                   290                  295                  300  
 Asp Ala Leu Leu Asp Leu Leu Lys Ser Lys Tyr Thr Gln Leu His Asp  
                   305                  310                  315                  320  
 Phe Gly Ser Glu Ile Leu Pro Arg Ala Val Leu Asp Phe Ser Val Gln  
                   325                  330                  335  
 Ala Cys Ile Phe Thr Gly Tyr Trp Glu Asp Val Gly Thr Ile Lys Ser  
                   340                  345                  350  
 Phe Phe Asp Ala Asn Leu Ala Leu Thr Glu Gln Pro Ser Lys Phe Asp  
                   355                  360                  365  
 Phe Tyr Asp Pro Lys Thr Pro Phe Phe Thr Ala Pro Arg Cys Leu Pro  
                   370                  375                  380  
 Pro Thr Gln Leu Asp Lys Cys Lys Met Lys Tyr Ala Phe Ile Ser Asp  
                   385                  390                  395                  400  
 Gly Cys Leu Leu Arg Glu Cys Asn Ile Glu His Ser Val Ile Gly Val  
                   405                  410                  415  
 Cys Ser Arg Val Ser Ser Gly Cys Glu Leu Lys Asp Ser Val Met Met  
                   420                  425                  430  
 Gly Ala Asp Ile Tyr Glu Thr Glu Glu Ala Ser Lys Leu Leu Leu  
                   435                  440                  445  
 Ala Gly Lys Val Pro Val Gly Ile Gly Arg Asn Thr Lys Ile Arg Asn  
                   450                  455                  460

Cys Ile Ile Asp Met Asn Ala Arg Ile Gly Lys Asn Val Val Ile Thr  
 465 470 475 480

Asn Ser Lys Gly Ile Gln Glu Ala Asp His Pro Glu Glu Gly Tyr Tyr  
 485 490 495

Ile Arg Ser Gly Ile Val Val Ile Leu Lys Asn Ala Thr Ile Asn Asp  
 500 505 510

Gly Ser Val Ile  
 515

<210> 33  
<211> 1576  
<212> DNA  
<213> Zea mays

<220>  
<221> CDS  
<222> (10)...(1563)  
<223> Shrunken-2 gene revertant form, modified to be  
heat stable

<220>  
<221> variation  
<222> (267)  
<223> k = g or t; amino acid 86 = Ala.

<220>  
<221> variation  
<222> (1368)  
<223> r = a or g; amino acid 453 = Pro.

<220>  
<221> variation  
<222> (1572)  
<223> k = g or t.

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Met Gln Phe Ala Leu Ala Leu Asp Thr Asn Ser Gly Pro His  
1 5 10

cag ata aga tct tgt gag ggt gat ggg att gac agg ttg gaa aaa tta 99  
Gln Ile Arg Ser Cys Glu Gly Asp Gly Ile Asp Arg Leu Glu Lys Leu  
15 20 25 30

agt att ggg ggc aga aag cag gag aaa gct ttg aga aat agg tgc ttt 147  
Ser Ile Gly Gly Arg Lys Gln Glu Lys Ala Leu Arg Asn Arg Cys Phe  
35 40 45

ggt ggt aga gtt gct gca act aca caa tgt att ctt acc tca gat gct 195  
Gly Gly Arg Val Ala Ala Thr Thr Gln Cys Ile Leu Thr Ser Asp Ala  
50 55 60

tgt cct gaa act ctt cat tct caa aca cag tcc tct agg aaa aat tat Cys Pro Glu Thr Leu His Ser Gln Thr Gln Ser Ser Arg Lys Asn Tyr 65 70 75	243
gct gat gca aac cgt gta tct gck atc att ttg ggc gga ggc act gga Ala Asp Ala Asn Arg Val Ser Ala Ile Ile Leu Gly Gly Gly Thr Gly 80 85 90	291
tct cag ctc ttt cct ctg aca agc aca aca gct acg cct gct gta cct Ser Gln Leu Phe Pro Leu Thr Ser Thr Arg Ala Thr Pro Ala Val Pro 95 100 105 110	339
gtt gga gga tgt tac agg ctt att gat atc cct atg agt aac tgc ttc Val Gly Gly Cys Tyr Arg Leu Ile Asp Ile Pro Met Ser Asn Cys Phe 115 120 125	387
aac agt ggt ata aat aag ata ttt gtg atg agt cag ttc aat tct act Asn Ser Gly Ile Asn Lys Ile Phe Val Met Ser Gln Phe Asn Ser Thr 130 135 140	435
tcg ctt aac cgc cat att cat cgt aca tac ctt gaa ggc ggg atc aac Ser Leu Asn Arg His Ile His Arg Thr Tyr Leu Glu Gly Ile Asn 145 150 155	483
ttt gct gat gga tct gta cag gta tta gcg gct aca caa atg cct gaa Phe Ala Asp Gly Ser Val Gln Val Leu Ala Ala Thr Gln Met Pro Glu 160 165 170	531
gag cca gct gga tgg ttc cag ggt aca gca gac tct atc aga aaa ttt Glu Pro Ala Gly Trp Phe Gln Gly Thr Ala Asp Ser Ile Arg Lys Phe 175 180 185 190	579
atc tgg gta ctc gag gat tat tac agt cac aaa tcc att gac aac att Ile Trp Val Leu Glu Asp Tyr Tyr Ser His Lys Ser Ile Asp Asn Ile 195 200 205	627
gta atc ttg agt ggc gat cag ctt tat cgg atg aat tac atg gaa ctt Val Ile Leu Ser Gly Asp Gln Leu Tyr Arg Met Asn Tyr Met Glu Leu 210 215 220	675
gtg cag aaa cat gtc gag gac gat gct gat atc act ata tca tgt gct Val Gln Lys His Val Glu Asp Asp Ala Asp Ile Thr Ile Ser Cys Ala 225 230 235	723
cct gtt gat gag agc cga gct tct aaa aat ggg cta gtg aag att gat Pro Val Asp Glu Ser Arg Ala Ser Lys Asn Gly Leu Val Lys Ile Asp 240 245 250	771
cat act gga cgt gta ctt caa ttc ttt gaa aaa cca aag ggt gct gat His Thr Gly Arg Val Leu Gln Phe Phe Glu Lys Pro Lys Gly Ala Asp 255 260 265 270	819
ttg aat tct atg aga gtt gag acc aac ttc ctg agc tat gct ata gat Leu Asn Ser Met Arg Val Glu Thr Asn Phe Leu Ser Tyr Ala Ile Asp 275 280 285	867
gat gca cag aaa tat cca tac ctt gca tca atg ggc att tat gtc ttc	915

Asp Ala Gln Lys Tyr Pro Tyr Leu Ala Ser Met Gly Ile Tyr Val Phe 290 295 300	
aag aaa gat gca ctt tta gac ctt ctc aag tca aaa tat act caa tta Lys Lys Asp Ala Leu Leu Asp Leu Leu Lys Ser Lys Tyr Thr Gln Leu 305 310 315	963
cat gac ttt gga tct gaa atc ctc cca aga gct gta cta gat atg agt His Asp Phe Gly Ser Glu Ile Leu Pro Arg Ala Val Leu Asp Met Ser 320 325 330	1011
gtg cag gca tgc att ttt acg ggc tat tgg gag gat gtt gga aca atc Val Gln Ala Cys Ile Phe Thr Gly Tyr Trp Glu Asp Val Gly Thr Ile 335 340 345 350	1059
aaa tca ttc ttt gat gca aac ttg gcc ctc act gag cag cct tcc aag Lys Ser Phe Asp Ala Asn Leu Ala Leu Thr Glu Gln Pro Ser Lys 355 360 365	1107
ttt gat ttt tac gat cca aaa aca cct ttc ttc act gca ccc cga tgc Phe Asp Phe Tyr Asp Pro Lys Thr Pro Phe Phe Thr Ala Pro Arg Cys 370 375 380	1155
ttg cct ccg acg caa ttg gac aag tgc aag atg aaa tat gca ttt atc Leu Pro Pro Thr Gln Leu Asp Lys Cys Lys Met Lys Tyr Ala Phe Ile 385 390 395	1203
tca gat ggt tgc tta ctg aga gaa tgc aac atc gag cat tct gtg att Ser Asp Gly Cys Leu Leu Arg Glu Cys Asn Ile Glu His Ser Val Ile 400 405 410	1251
ggg gtc tgc tca cgt gtc agc tct gga tgt gaa ctc aag gac tcc gtg Gly Val Cys Ser Arg Val Ser Ser Gly Cys Glu Leu Lys Asp Ser Val 415 420 425 430	1299
atg atg gga gcg gac atc tat gaa act gaa gaa gaa gct tca aag cta Met Met Gly Ala Asp Ile Tyr Glu Thr Glu Glu Ala Ser Lys Leu 435 440 445	1347
ctg tta gct ggg aag gtc ccr gtt gga ata gga agg aac aca aag ata Leu Leu Ala Gly Lys Val Pro Val Gly Ile Gly Arg Asn Thr Lys Ile 450 455 460	1395
agg aac tgt atc att gac atg aat gct agg att ggg aag aac gtg gtg Arg Asn Cys Ile Ile Asp Met Asn Ala Arg Ile Gly Lys Asn Val Val 465 470 475	1443
atc aca aac agt aag ggc atc caa gag gct gat cac ccg gaa gaa ggg Ile Thr Asn Ser Lys Gly Ile Gln Glu Ala Asp His Pro Glu Glu Gly 480 485 490	1491
tac tac ata agg tct gga atc gtg gtg atc ctg aag aat gca acc atc Tyr Tyr Ile Arg Ser Gly Ile Val Val Ile Leu Lys Asn Ala Thr Ile 495 500 505 510	1539
aac gat ggg tct gtc ata tagatcggtc gcgatkgtcg Asn Asp Gly Ser Val Ile	1576

515

<210> 34  
<211> 516  
<212> PRT  
<213> Zea mays

&lt;400&gt; 34

Met	Gln	Phe	Ala	Leu	Ala	Leu	Asp	Thr	Asn	Ser	Gly	Pro	His	Gln	Ile
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Arg	Ser	Cys	Glu	Gly	Asp	Gly	Ile	Asp	Arg	Leu	Glu	Lys	Leu	Ser	Ile
		20					25					30			
Gly	Gly	Arg	Lys	Gln	Glu	Lys	Ala	Leu	Arg	Asn	Arg	Cys	Phe	Gly	Gly
	35						40				45				
Arg	Val	Ala	Ala	Thr	Thr	Gln	Cys	Ile	Leu	Thr	Ser	Asp	Ala	Cys	Pro
	50					55				60					
Glu	Thr	Leu	His	Ser	Gln	Thr	Gln	Ser	Ser	Arg	Lys	Asn	Tyr	Ala	Asp
	65					70				75					80
Ala	Asn	Arg	Val	Ser	Ala	Ile	Ile	Leu	Gly	Gly	Gly	Thr	Gly	Ser	Gln
					85			90					95		
Leu	Phe	Pro	Leu	Thr	Ser	Thr	Arg	Ala	Thr	Pro	Ala	Val	Pro	Val	Gly
		100					105					110			
Gly	Cys	Tyr	Arg	Leu	Ile	Asp	Ile	Pro	Met	Ser	Asn	Cys	Phe	Asn	Ser
	115					120					125				
Gly	Ile	Asn	Lys	Ile	Phe	Val	Met	Ser	Gln	Phe	Asn	Ser	Thr	Ser	Leu
	130					135					140				
Asn	Arg	His	Ile	His	Arg	Thr	Tyr	Leu	Glu	Gly	Ile	Asn	Phe	Ala	
	145					150			155			160			
Asp	Gly	Ser	Val	Gln	Val	Leu	Ala	Ala	Thr	Gln	Met	Pro	Glu	Glu	Pro
			165						170			175			
Ala	Gly	Trp	Phe	Gln	Gly	Thr	Ala	Asp	Ser	Ile	Arg	Lys	Phe	Ile	Trp
		180					185					190			
Val	Leu	Glu	Asp	Tyr	Tyr	Ser	His	Lys	Ser	Ile	Asp	Asn	Ile	Val	Ile
		195					200					205			
Leu	Ser	Gly	Asp	Gln	Leu	Tyr	Arg	Met	Asn	Tyr	Met	Glu	Leu	Val	Gln
	210					215				220					
Lys	His	Val	Glu	Asp	Asp	Ala	Asp	Ile	Thr	Ile	Ser	Cys	Ala	Pro	Val
	225					230				235			240		
Asp	Glu	Ser	Arg	Ala	Ser	Lys	Asn	Gly	Leu	Val	Lys	Ile	Asp	His	Thr
		245					250					255			

Gly Arg Val Leu Gln Phe Phe Glu Lys Pro Lys Gly Ala Asp Leu Asn  
                  260                       265                       270  
 Ser Met Arg Val Glu Thr Asn Phe Leu Ser Tyr Ala Ile Asp Asp Ala  
                  275                       280                       285  
 Gln Lys Tyr Pro Tyr Leu Ala Ser Met Gly Ile Tyr Val Phe Lys Lys  
                  290                       295                       300  
 Asp Ala Leu Leu Asp Leu Leu Lys Ser Lys Tyr Thr Gln Leu His Asp  
                  305                       310                       315                       320  
 Phe Gly Ser Glu Ile Leu Pro Arg Ala Val Leu Asp Met Ser Val Gln  
                  325                       330                       335  
 Ala Cys Ile Phe Thr Gly Tyr Trp Glu Asp Val Gly Thr Ile Lys Ser  
                  340                       345                       350  
 Phe Phe Asp Ala Asn Leu Ala Leu Thr Glu Gln Pro Ser Lys Phe Asp  
                  355                       360                       365  
 Phe Tyr Asp Pro Lys Thr Pro Phe Phe Thr Ala Pro Arg Cys Leu Pro  
                  370                       375                       380  
 Pro Thr Gln Leu Asp Lys Cys Lys Met Lys Tyr Ala Phe Ile Ser Asp  
                  385                       390                       395                       400  
 Gly Cys Leu Leu Arg Glu Cys Asn Ile Glu His Ser Val Ile Gly Val  
                  405                       410                       415  
 Cys Ser Arg Val Ser Ser Gly Cys Glu Leu Lys Asp Ser Val Met Met  
                  420                       425                       430  
 Gly Ala Asp Ile Tyr Glu Thr Glu Glu Ala Ser Lys Leu Leu Leu  
                  435                       440                       445  
 Ala Gly Lys Val Pro Val Gly Ile Gly Arg Asn Thr Lys Ile Arg Asn  
                  450                       455                       460  
 Cys Ile Ile Asp Met Asn Ala Arg Ile Gly Lys Asn Val Val Ile Thr  
                  465                       470                       475                       480  
 Asn Ser Lys Gly Ile Gln Glu Ala Asp His Pro Glu Glu Gly Tyr Tyr  
                  485                       490                       495  
 Ile Arg Ser Gly Ile Val Val Ile Leu Lys Asn Ala Thr Ile Asn Asp  
                  500                       505                       510  
 Gly Ser Val Ile  
                  515

<210> 35  
 <211> 1576  
 <212> DNA  
 <213> Zea mays

<220>  
 <221> CDS  
 <222> (10)..(1563)  
 <223> Shrunken-2 gene revertant form, modified to be  
 heat stable

<220>  
 <221> variation  
 <222> (267)  
 <223> k = g or t; amino acid 86 = Ala.

<220>  
 <221> variation  
 <222> (540)  
 <223> n = a or g or c or t/u, unknown, or other.

<220>  
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 <222> (1008)  
 <223> y = c or t.

<220>  
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 <222> (1368)  
 <223> r = a or g; amino acid 453 = Pro.

<220>  
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 <223> k = g or t.

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 Met Gln Phe Ala Leu Ala Leu Asp Thr Asn Ser Gly Pro His  
       1                  5   10

cag ata aga tct tgt gag ggt gat ggg att gac agg ttg gaa aaa tta	99
Gln Ile Arg Ser Cys Glu Gly Asp Gly Ile Asp Arg Leu Glu Lys Leu	
15   30	

att ggg ggc aga aag cag gag aaa gct ttg aga aat agg tgc ttt	147
Ser Ile Gly Gly Arg Lys Gln Glu Lys Ala Leu Arg Asn Arg Cys Phe	
35   45	

ggt ggt aga gtt gct gca act aca caa tgt att ctt acc tca gat gct	195
Gly Gly Arg Val Ala Ala Thr Thr Gln Cys Ile Leu Thr Ser Asp Ala	
50   60	

tgt cct gaa act ctt cat tct caa aca cag tcc tct agg aaa aat tat	243
Cys Pro Glu Thr Leu His Ser Gln Thr Gln Ser Ser Arg Lys Asn Tyr	
65   75	

gct gat gca aac cgt gta tct gck atc att ttg ggc gga ggc act gga	291
Ala Asp Ala Asn Arg Val Ser Ala Ile Ile Leu Gly Gly Thr Gly	
80   90	

tct cag ctc ttt cct ctg aca agc aca aga gct acg cct gct gta cct	339
Ser Gln Leu Phe Pro Leu Thr Ser Thr Arg Ala Thr Pro Ala Val Pro	
95 100 105 110	
gtt gga gga tgt tac agg ctt att gat atc cct atg agt aac tgc ttc	387
Val Gly Gly Cys Tyr Arg Leu Ile Asp Ile Pro Met Ser Asn Cys Phe	
115 120 125	
aac agt ggt ata aat aag ata ttt gtg atg agt cag ttc aat tct act	435
Asn Ser Gly Ile Asn Lys Ile Phe Val Met Ser Gln Phe Asn Ser Thr	
130 135 140	
tcg ctt aac cgc cat att cat cgt aca tac ctt gaa ggc ggg atc aac	483
Ser Leu Asn Arg His Ile His Arg Thr Tyr Leu Glu Gly Gly Ile Asn	
145 150 155	
ttt gct gat gga tct gta cag gta tta gcg gct aca caa atg cct gaa	531
Phe Ala Asp Gly Ser Val Gln Val Leu Ala Ala Thr Gln Met Pro Glu	
160 165 170	
gag cca gtn gga tgg ttc cag ggt aca gca gac tct atc aga aaa ttt	579
Glu Pro Val Gly Trp Phe Gln Gly Thr Ala Asp Ser Ile Arg Lys Phe	
175 180 185 190	
atc tgg gta ctc gag gat tat tac agt cac aaa tcc att gac aac att	627
Ile Trp Val Leu Glu Asp Tyr Tyr Ser His Lys Ser Ile Asp Asn Ile	
195 200 205	
gta atc ttg agt ggc gat cag ctt tat cgg atg aat tac atg gaa ctt	675
Val Ile Leu Ser Gly Asp Gln Leu Tyr Arg Met Asn Tyr Met Glu Leu	
210 215 220	
gtg cag aaa cat gtc gag gac gat gct gat atc act ata tca tgt gct	723
Val Gln Lys His Val Glu Asp Ala Asp Ile Thr Ile Ser Cys Ala	
225 230 235	
cct gtt gat gag agc cga gct tct aaa aat ggg cta gtg aag att gat	771
Pro Val Asp Glu Ser Arg Ala Ser Lys Asn Gly Leu Val Lys Ile Asp	
240 245 250	
cat act gga cgt gta ctt caa ttc ttt gaa aaa cca aag ggt gct gat	819
His Thr Gly Arg Val Leu Gln Phe Phe Glu Lys Pro Lys Gly Ala Asp	
255 260 265 270	
ttg aat tct atg aga gtt gag acc aac ttc ctg agc tat gct ata gat	867
Leu Asn Ser Met Arg Val Glu Thr Asn Phe Leu Ser Tyr Ala Ile Asp	
275 280 285	
gat gca cag aaa tat cca tac ctt gca tca atg ggc att tat gtc ttc	915
Asp Ala Gln Lys Tyr Pro Tyr Leu Ala Ser Met Gly Ile Tyr Val Phe	
290 295 300	
aag aaa gat gca ctt tta gac ctt ctc aag tca aaa tat act caa tta	963
Lys Lys Asp Ala Leu Leu Asp Leu Leu Lys Ser Lys Tyr Thr Gln Leu	
305 310 315	
cat gac ttt gga tct gaa atc ctc cca aga gct gta cta gat tay agt	1011

His Asp Phe Gly Ser Glu Ile Leu Pro Arg Ala Val Leu Asp Tyr Ser		
320	325	330
gtg cag gca tgc att ttt acg ggc tat tgg gag gat gtt gga aca atc		1059
Val Gln Ala Cys Ile Phe Thr Gly Tyr Trp Glu Asp Val Gly Thr Ile		
335	340	345
aaa tca ttc ttt gat gca aac ttg gcc ctc act gag cag cct tcc aag		1107
Lys Ser Phe Phe Asp Ala Asn Leu Ala Leu Thr Glu Gln Pro Ser Lys		
355	360	365
ttt gat ttt tac gat cca aaa aca cct ttc ttc act gca ccc cga tgc		1155
Phe Asp Phe Tyr Asp Pro Lys Thr Pro Phe Phe Thr Ala Pro Arg Cys		
370	375	380
ttg cct ccg acg caa ttg gac aag tgc aag atg aaa tat gca ttt atc		1203
Leu Pro Pro Thr Gln Leu Asp Lys Cys Lys Met Lys Tyr Ala Phe Ile		
385	390	395
tca gat ggt tgc tta ctg aga gaa tgc aac atc gag cat tct gtg att		1251
Ser Asp Gly Cys Leu Leu Arg Glu Cys Asn Ile Glu His Ser Val Ile		
400	405	410
gga gtc tgc tca cgt gtc agc tct gga tgt gaa ctc aag gac tcc gtg		1299
Gly Val Cys Ser Arg Val Ser Ser Gly Cys Glu Leu Lys Asp Ser Val		
415	420	425
atg atg gga gcg gac atc tat gaa act gaa gaa gaa gct tca aag cta		1347
Met Met Gly Ala Asp Ile Tyr Glu Thr Glu Glu Ala Ser Lys Leu		
435	440	445
ctg tta gct ggg aag gtc ccr gtt gga ata gga agg aac aca aag ata		1395
Leu Leu Ala Gly Lys Val Pro Val Gly Ile Gly Arg Asn Thr Lys Ile		
450	455	460
agg aac tgt atc att gac atg aat gct agg att ggg aag aac gtg gtg		1443
Arg Asn Cys Ile Ile Asp Met Asn Ala Arg Ile Gly Lys Asn Val Val		
465	470	475
atc aca aac agt aag ggc atc caa gag gct gat cac ccg gaa gaa ggg		1491
Ile Thr Asn Ser Lys Gly Ile Gln Glu Ala Asp His Pro Glu Glu Gly		
480	485	490
tac tac ata agg tct gga atc gtg gtg atc ctg aag aat gca acc atc		1539
Tyr Tyr Ile Arg Ser Gly Ile Val Val Ile Leu Lys Asn Ala Thr Ile		
495	500	505
aac gat ggg tct gtc ata tagatcggt gcgtktgcg		1576
Asn Asp Gly Ser Val Ile		
515		

<210> 36  
<211> 516  
<212> PRT  
<213> Zea mays

&lt;400&gt; 36

Met Gln Phe Ala Leu Ala Leu Asp Thr Asn Ser Gly Pro His Gln Ile			
1	5	10	15
Arg Ser Cys Glu Gly Asp Gly Ile Asp Arg Leu Glu Lys Leu Ser Ile			
20	25	30	
Gly Gly Arg Lys Gln Glu Lys Ala Leu Arg Asn Arg Cys Phe Gly Gly			
35	40	45	
Arg Val Ala Ala Thr Thr Gln Cys Ile Leu Thr Ser Asp Ala Cys Pro			
50	55	60	
Glu Thr Leu His Ser Gln Thr Gln Ser Ser Arg Lys Asn Tyr Ala Asp			
65	70	75	80
Ala Asn Arg Val Ser Ala Ile Ile Leu Gly Gly Gly Thr Gly Ser Gln			
85	90	95	
Leu Phe Pro Leu Thr Ser Thr Arg Ala Thr Pro Ala Val Pro Val Gly			
100	105	110	
Gly Cys Tyr Arg Leu Ile Asp Ile Pro Met Ser Asn Cys Phe Asn Ser			
115	120	125	
Gly Ile Asn Lys Ile Phe Val Met Ser Gln Phe Asn Ser Thr Ser Leu			
130	135	140	
Asn Arg His Ile His Arg Thr Tyr Leu Glu Gly Gly Ile Asn Phe Ala			
145	150	155	160
Asp Gly Ser Val Gln Val Leu Ala Ala Thr Gln Met Pro Glu Glu Pro			
165	170	175	
Val Gly Trp Phe Gln Gly Thr Ala Asp Ser Ile Arg Lys Phe Ile Trp			
180	185	190	
Val Leu Glu Asp Tyr Tyr Ser His Lys Ser Ile Asp Asn Ile Val Ile			
195	200	205	
Leu Ser Gly Asp Gln Leu Tyr Arg Met Asn Tyr Met Glu Leu Val Gln			
210	215	220	
Lys His Val Glu Asp Asp Ala Asp Ile Thr Ile Ser Cys Ala Pro Val			
225	230	235	240
Asp Glu Ser Arg Ala Ser Lys Asn Gly Leu Val Lys Ile Asp His Thr			
245	250	255	
Gly Arg Val Leu Gln Phe Phe Glu Lys Pro Lys Gly Ala Asp Leu Asn			
260	265	270	
Ser Met Arg Val Glu Thr Asn Phe Leu Ser Tyr Ala Ile Asp Asp Ala			
275	280	285	
Gln Lys Tyr Pro Tyr Leu Ala Ser Met Gly Ile Tyr Val Phe Lys Lys			

290	295	300
Asp Ala Leu Leu Asp Leu Leu Lys Ser Lys Tyr Thr Gln Leu His Asp		
305	310	315
Phe Gly Ser Glu Ile Leu Pro Arg Ala Val Leu Asp Tyr Ser Val Gln		
325	330	335
Ala Cys Ile Phe Thr Gly Tyr Trp Glu Asp Val Gly Thr Ile Lys Ser		
340	345	350
Phe Phe Asp Ala Asn Leu Ala Leu Thr Glu Gln Pro Ser Lys Phe Asp		
355	360	365
Phe Tyr Asp Pro Lys Thr Pro Phe Phe Thr Ala Pro Arg Cys Leu Pro		
370	375	380
Pro Thr Gln Leu Asp Lys Cys Lys Met Lys Tyr Ala Phe Ile Ser Asp		
385	390	395
Gly Cys Leu Leu Arg Glu Cys Asn Ile Glu His Ser Val Ile Gly Val		
405	410	415
Cys Ser Arg Val Ser Ser Gly Cys Glu Leu Lys Asp Ser Val Met Met		
420	425	430
Gly Ala Asp Ile Tyr Glu Thr Glu Glu Ala Ser Lys Leu Leu Leu		
435	440	445
Ala Gly Lys Val Pro Val Gly Ile Gly Arg Asn Thr Lys Ile Arg Asn		
450	455	460
Cys Ile Ile Asp Met Asn Ala Arg Ile Gly Lys Asn Val Val Ile Thr		
465	470	475
Asn Ser Lys Gly Ile Gln Glu Ala Asp His Pro Glu Glu Gly Tyr Tyr		
485	490	495
Ile Arg Ser Gly Ile Val Val Ile Leu Lys Asn Ala Thr Ile Asn Asp		
500	505	510
Gly Ser Val Ile		
515		

<210> 37  
<211> 1576  
<212> DNA  
<213> Zea mays

<220>  
<221> CDS  
<222> (10)..(1563)  
<223> Shrunken-2 gene revertant form, modified to be  
heat stable

<220>

<221> variation  
 <222> (267)  
 <223> k = g or t; amino acid 86 = Ala.

<220>  
 <221> variation  
 <222> (1008)  
 <223> y = c or t.

<220>  
 <221> variation  
 <222> (1197)  
 <223> n = a or g or c or t/u, unknown, or other.

<220>  
 <221> variation  
 <222> (1368)  
 <223> r = a or g; amino acid 453 = Pro.

<220>  
 <221> variation  
 <222> (1572)  
 <223> k = g or t.

<400> 37  
 ggaggagat atg cag ttt gca ctt gca ttg gac acg aac tca ggt cct cac 51  
 Met Gln Phe Ala Leu Ala Leu Asp Thr Asn Ser Gly Pro His  
 1 5 10

cag ata aga tct tgt gag ggt gat ggg att gac agg ttg gaa aaa tta 99  
 Gln Ile Arg Ser Cys Glu Gly Asp Gly Ile Asp Arg Leu Glu Lys Ile  
 15 20 25 30

agt att ggg ggc aga aag cag gag aaa gct ttg aga aat agg tgc ttt 147  
 Ser Ile Gly Gly Arg Lys Glu Lys Ala Leu Arg Asn Arg Cys Phe  
 35 40 45

ggg ggt aga gtt gct gca act aca caa tgt att ctt acc tca gat gct 195  
 Gly Gly Arg Val Ala Ala Thr Thr Gln Cys Ile Leu Thr Ser Asp Ala  
 50 55 60

tgt cct gaa act ctt cat tct caa aca cag tcc tct agg aaa aat tat 243  
 Cys Pro Glu Thr Leu His Ser Gln Thr Gln Ser Ser Arg Lys Asn Tyr  
 65 70 75

gct gat gca aac cgt gta tct gck atc att ttg ggc gga ggc act gga 291  
 Ala Asp Ala Asn Arg Val Ser Ala Ile Ile Leu Gly Gly Gly Thr Gly  
 80 85 90

tct cag ctc ttt cct ctg aca agc aca aga gct acg cct gct gta cct 339  
 Ser Gln Leu Phe Pro Leu Thr Ser Thr Arg Ala Thr Pro Ala Val Pro  
 95 100 105 110

gtt gga gga tgt tac agg ctt att gat atc cct atg agt aac tgc ttc 387  
 Val Gly Gly Cys Tyr Arg Leu Ile Asp Ile Pro Met Ser Asn Cys Phe  
 115 120 125

aac agt ggt ata aat aag ata ttt gtg atg agt cag ttc aat tct act Asn Ser Gly Ile Asn Lys Ile Phe Val Met Ser Gln Phe Asn Ser Thr 130 135 140	435
tcg ctt aac cgc cat att cat cgt aca tac ctt gaa ggc ggg atc aac Ser Leu Asn Arg His Ile His Arg Thr Tyr Leu Glu Gly Gly Ile Asn 145 150 155	483
ttt gct gat gga tct gta cag gta tta gcg gct aca caa atg cct gaa Phe Ala Asp Gly Ser Val Gln Val Leu Ala Ala Thr Gln Met Pro Glu 160 165 170	531
gag cca gct gga tgg ttc cag ggt aca gca gac tct atc aga aaa ttt Glu Pro Ala Gly Trp Phe Gln Gly Thr Ala Asp Ser Ile Arg Lys Phe 175 180 185 190	579
atc tgg gta ctc gag gat tat tac agt cac aaa tcc att gac aac att Ile Trp Val Leu Glu Asp Tyr Tyr Ser His Lys Ser Ile Asp Asn Ile 195 200 205	627
gta atc ttg agt ggc gat cag ctt tat cgg atg aat tac atg gaa ctt Val Ile Leu Ser Gly Asp Gln Leu Tyr Arg Met Asn Tyr Met Glu Leu 210 215 220	675
gtg cag aaa cat gtc gag gac gat gct gat atc act ata tca tgt gct Val Gln Lys His Val Glu Asp Asp Ala Asp Ile Thr Ile Ser Cys Ala 225 230 235	723
cct gtt gat gag agc cga gct tct aaa aat ggg cta gtg aag att gat Pro Val Asp Glu Ser Arg Ala Ser Lys Asn Gly Leu Val Lys Ile Asp 240 245 250	771
cat act gga cgt gta ctt caa ttc ttt gaa aaa cca aag ggt gct gat His Thr Gly Arg Val Leu Gln Phe Phe Glu Lys Pro Lys Gly Ala Asp 255 260 265 270	819
ttg aat tct atg aga gtt gag acc aac ttc ctg agc tat gct ata gat Leu Asn Ser Met Arg Val Glu Thr Asn Phe Leu Ser Tyr Ala Ile Asp 275 280 285	867
gat gca cag aaa tat cca tac ctt gca tca atg ggc att tat gtc ttc Asp Ala Gln Lys Tyr Pro Tyr Leu Ala Ser Met Gly Ile Tyr Val Phe 290 295 300	915
aag aaa gat gca ctt tta gac ctt ctc aag tca aaa tat act caa tta Lys Lys Asp Ala Leu Leu Asp Leu Leu Lys Ser Lys Tyr Thr Gln Leu 305 310 315	963
cat gac ttt gga tct gaa atc ctc cca aga gct gta cta gat tay agt His Asp Phe Gly Ser Glu Ile Leu Pro Arg Ala Val Leu Asp Tyr Ser 320 325 330	1011
gtg cag gca tgc att ttt acg ggc tat tgg gag gat gtt gga aca atc Val Gln Ala Cys Ile Phe Thr Gly Tyr Trp Glu Asp Val Gly Thr Ile 335 340 345 350	1059
aaa tca ttc ttt gat gca aac ttg gcc ctc act gag cag cct tcc aag	1107

Lys Ser Phe Phe Asp Ala Asn Leu Ala Leu Thr Glu Gln Pro Ser Lys 355	360	365	
ttt gat ttt tac gat cca aaa aca cct ttc ttc act gca ccc cga tgc Phe Asp Phe Tyr Asp Pro Lys Thr Pro Phe Thr Ala Pro Arg Cys 370	375	380	1155
ttg cct ccg acg caa ttg gac aag tgc aag atg aaa tat gtn ttt atc Leu Pro Pro Thr Gln Leu Asp Lys Cys Lys Met Lys Tyr Val Phe Ile 385	390	395	1203
tca gat ggt tgc tta ctg aga gaa tgc aac atc gag cat tct gtg att Ser Asp Gly Cys Leu Leu Arg Glu Cys Asn Ile Glu His Ser Val Ile 400	405	410	1251
gga gtc tgc tca cgt gtc agc tct gga tgt gaa ctc aag gac tcc gtg Gly Val Cys Ser Arg Val Ser Ser Gly Cys Glu Leu Lys Asp Ser Val 415	420	425	1299
atg atg gga gcg gac atc tat gaa act gaa gaa gaa gct tca aag cta Met Met Gly Ala Asp Ile Tyr Glu Thr Glu Glu Glu Ala Ser Lys Leu 435	440	445	1347
ctg tta gct ggg aag gtc ccr gtt gga ata gga agg aac aca aag ata Leu Leu Ala Gly Lys Val Pro Val Gly Ile Gly Arg Asn Thr Lys Ile 450	455	460	1395
agg aac tgt atc att gac atg aat gct agg att ggg aag aac gtg gtg Arg Asn Cys Ile Ile Asp Met Asn Ala Arg Ile Gly Lys Asn Val Val 465	470	475	1443
atc aca aac agt aag ggc atc caa gag gct gat cac ccg gaa gaa ggg Ile Thr Asn Ser Lys Gly Ile Gln Glu Ala Asp His Pro Glu Glu Gly 480	485	490	1491
tac tac ata agg tct gga atc gtg gtg atc ctg aag aat gca acc atc Tyr Tyr Ile Arg Ser Gly Ile Val Val Ile Leu Lys Asn Ala Thr Ile 495	500	505	1539
aac gat ggg tct gtc ata tagatccgt gcgtktgcg Asn Asp Gly Ser Val Ile 515			1576
<210> 38 <211> 516 <212> PRT <213> Zea mays			
<400> 38			
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Arg Ser Cys Glu Gly Asp Gly Ile Asp Arg Leu Glu Lys Leu Ser Ile 20 25 30			

Gly Gly Arg Lys Gln Glu Lys Ala Leu Arg Asn Arg Cys Phe Gly Gly  
 35 40 45  
 Arg Val Ala Ala Thr Thr Gln Cys Ile Leu Thr Ser Asp Ala Cys Pro  
 50 55 60  
 Glu Thr Leu His Ser Gln Thr Gln Ser Ser Arg Lys Asn Tyr Ala Asp  
 65 70 75 80  
 Ala Asn Arg Val Ser Ala Ile Ile Leu Gly Gly Gly Thr Gly Ser Gln  
 85 90 95  
 Leu Phe Pro Leu Thr Ser Thr Arg Ala Thr Pro Ala Val Pro Val Gly  
 100 105 110  
 Gly Cys Tyr Arg Leu Ile Asp Ile Pro Met Ser Asn Cys Phe Asn Ser  
 115 120 125  
 Gly Ile Asn Lys Ile Phe Val Met Ser Gln Phe Asn Ser Thr Ser Leu  
 130 135 140  
 Asn Arg His Ile His Arg Thr Tyr Leu Glu Gly Ile Asn Phe Ala  
 145 150 155 160  
 Asp Gly Ser Val Gln Val Leu Ala Ala Thr Gln Met Pro Glu Glu Pro  
 165 170 175  
 Ala Gly Trp Phe Gln Gly Thr Ala Asp Ser Ile Arg Lys Phe Ile Trp  
 180 185 190  
 Val Leu Glu Asp Tyr Tyr Ser His Lys Ser Ile Asp Asn Ile Val Ile  
 195 200 205  
 Leu Ser Gly Asp Gln Leu Tyr Arg Met Asn Tyr Met Glu Leu Val Gln  
 210 215 220  
 Lys His Val Glu Asp Asp Ala Asp Ile Thr Ile Ser Cys Ala Pro Val  
 225 230 235 240  
 Asp Glu Ser Arg Ala Ser Lys Asn Gly Leu Val Lys Ile Asp His Thr  
 245 250 255  
 Gly Arg Val Leu Gln Phe Phe Glu Lys Pro Lys Gly Ala Asp Leu Asn  
 260 265 270  
 Ser Met Arg Val Glu Thr Asn Phe Leu Ser Tyr Ala Ile Asp Asp Ala  
 275 280 285  
 Gln Lys Tyr Pro Tyr Leu Ala Ser Met Gly Ile Tyr Val Phe Lys Lys  
 290 295 300  
 Asp Ala Leu Leu Asp Leu Leu Lys Ser Lys Tyr Thr Gln Leu His Asp  
 305 310 315 320  
 Phe Gly Ser Glu Ile Leu Pro Arg Ala Val Leu Asp Tyr Ser Val Gln  
 325 330 335

Ala Cys Ile Phe Thr Gly Tyr Trp Glu Asp Val Gly Thr Ile Lys Ser  
 340 345 350  
 Phe Phe Asp Ala Asn Leu Ala Leu Thr Glu Gln Pro Ser Lys Phe Asp  
 355 360 365  
 Phe Tyr Asp Pro Lys Thr Pro Phe Phe Thr Ala Pro Arg Cys Leu Pro  
 370 375 380  
 Pro Thr Gln Leu Asp Lys Cys Lys Met Lys Tyr Val Phe Ile Ser Asp  
 385 390 395 400  
 Gly Cys Leu Leu Arg Glu Cys Asn Ile Glu His Ser Val Ile Gly Val  
 405 410 415  
 Cys Ser Arg Val Ser Ser Gly Cys Glu Leu Lys Asp Ser Val Met Met  
 420 425 430  
 Gly Ala Asp Ile Tyr Glu Thr Glu Glu Ala Ser Lys Leu Leu Leu  
 435 440 445  
 Ala Gly Lys Val Pro Val Gly Ile Gly Arg Asn Thr Lys Ile Arg Asn  
 450 455 460  
 Cys Ile Ile Asp Met Asn Ala Arg Ile Gly Lys Asn Val Val Ile Thr  
 465 470 475 480  
 Asn Ser Lys Gly Ile Gln Glu Ala Asp His Pro Glu Glu Gly Tyr Tyr  
 485 490 495  
 Ile Arg Ser Gly Ile Val Val Ile Leu Lys Asn Ala Thr Ile Asn Asp  
 500 505 510  
 Gly Ser Val Ile  
 515

<210> 39  
 <211> 1576  
 <212> DNA  
 <213> Zea mays  
  
 <220>  
 <221> CDS  
 <222> (10)..(1563)  
 <223> Shrunken-2 gene revertant form, modified to be  
 heat stable  
  
 <220>  
 <221> variation  
 <222> (267)  
 <223> k = g or t; amino acid 86 = Ala.  
  
 <220>  
 <221> variation  
 <222> (540)  
 <223> n = a or g or c or t/u, unknown, or other.

<220>  
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<222> (1008)  
<223> y = c or t.

<220>  
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<222> (1197)  
<223> n = a or g or c or t/u, unknown, or other.

<220>  
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<223> r = a or g; amino acid 453 = Pro.

<220>  
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<223> k = g or t.

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ggagggatg atg cag ttt gca ctt gca ttg gac acg aac tca ggt cct cac 51  
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1 5 10

cag ata aga tct tgt gag ggt gat ggg att gag ttg gaa aaa tta 99  
Gln Ile Arg Ser Cys Glu Gly Asp Gly Ile Asp Arg Leu Glu Lys Leu  
15 20 25 30

agt att ggg ggc aga aag cag gag aaa gct ttg aga aat agg tgc ttt 147  
Ser Ile Gly Arg Lys Gln Glu Lys Ala Leu Arg Asn Arg Cys Phe  
35 40 45

ggg ggt aga gtt gca act aca caa tgt att ctt acc tca gat gct 195  
Gly Gly Arg Val Ala Ala Thr Thr Gln Cys Ile Leu Thr Ser Asp Ala  
50 55 60

tgt cct gaa act ctt cat tct caa aca cag tcc tct agg aaa aat tat 243  
Cys Pro Glu Thr Leu His Ser Gln Thr Gln Ser Ser Arg Lys Asn Tyr  
65 70 75

gct gat gca aac cgt gta tct gck atc att ttg ggc gga ggc act gga 291  
Ala Asp Ala Asn Arg Val Ser Ala Ile Ile Leu Gly Gly Gly Thr Gly  
80 85 90

tct cag ctc ttt cct ctg aca agc aca aga gct acg cct gct gta cct 339  
Ser Gln Leu Phe Pro Leu Thr Ser Thr Arg Ala Thr Pro Ala Val Pro  
95 100 105 110

gtt gga gga tgt tac agg ctt att gat atc cct atg agt aac tgc ttc 387  
Val Gly Gly Cys Tyr Arg Leu Ile Asp Ile Pro Met Ser Asn Cys Phe  
115 120 125

aac agt ggt ata aat aag ata ttt gtg atg agt cag ttc aat tct act 435  
Asn Ser Gly Ile Asn Lys Ile Phe Val Met Ser Gln Phe Asn Ser Thr  
130 135 140

tcg ctt aac cgc cat att cat cgt aca tac ctt gaa ggc ggg atc aac Ser Leu Asn Arg His Ile His Arg Thr Tyr Leu Glu Gly Gly Ile Asn 145 150 155	483
ttt gct gat gga tct gta cag gta tta ggc gct aca caa atg cct gaa Phe Ala Asp Gly Ser Val Gln Val Leu Ala Ala Thr Gln Met Pro Glu 160 165 170	531
gag cca gtn gga tgg ttc cag ggt aca gca gac tct atc aga aaa ttt Glu Pro Val Gly Trp Phe Gln Gly Thr Ala Asp Ser Ile Arg Lys Phe 175 180 185 190	579
atc tgg gta ctc gag gat tat tac agt cac aaa tcc att gac aac att Ile Trp Val Leu Glu Asp Tyr Tyr Ser His Lys Ser Ile Asp Asn Ile 195 200 205	627
gta atc ttg agt ggc gat cag ctt tat cgg atg aat tac atg gaa ctt Val Ile Leu Ser Gly Asp Gln Leu Tyr Arg Met Asn Tyr Met Glu Leu 210 215 220	675
gtg cag aaa cat gtc gag gac gat gct gat atc act ata tca tgt gct Val Gln Lys His Val Glu Asp Asp Ala Asp Ile Thr Ile Ser Cys Ala 225 230 235	723
cct gtt gat gag agc cga gct tct aaa aat ggg cta gtg aag att gat Pro Val Asp Glu Ser Arg Ala Ser Lys Asn Gly Leu Val Lys Ile Asp 240 245 250	771
cat act gga cgt gta ctt caa ttc ttt gaa aaa cca aag ggt gct gat His Thr Gly Arg Val Leu Gln Phe Phe Glu Lys Pro Lys Gly Ala Asp 255 260 265 270	819
ttg aat tct atg aga gtt gag acc aac ttc ctg agc tat gct ata gat Leu Asn Ser Met Arg Val Glu Thr Asn Phe Leu Ser Tyr Ala Ile Asp 275 280 285	867
gat gca cag aaa tat cca tac ctt gca tca atg ggc att tat gtc ttc Asp Ala Gln Lys Tyr Pro Tyr Leu Ala Ser Met Gly Ile Tyr Val Phe 290 295 300	915
aag aaa gat gca ctt tta gac ctt ctc aag tca aaa tat act caa tta Lys Lys Asp Ala Leu Leu Asp Leu Leu Lys Ser Lys Tyr Thr Gln Leu 305 310 315	963
cat gac ttt gga tct gaa atc ctc cca aga gct gta cta gat cay agt His Asp Phe Gly Ser Glu Ile Leu Pro Arg Ala Val Leu Asp His Ser 320 325 330	1011
gtg cag gca tgc att ttt acg ggc tat tgg gag gat gtt gga aca atc Val Gln Ala Cys Ile Phe Thr Gly Tyr Trp Glu Asp Val Gly Thr Ile 335 340 345 350	1059
aaa tca ttc ttt gat gca aac ttg gcc ctc act gag cag cct tcc aag Lys Ser Phe Asp Ala Asn Leu Ala Leu Thr Glu Gln Pro Ser Lys 355 360 365	1107

ttt gat ttt tac gat cca aaa aca cct ttc ttc act gca ccc cga tgc 1155  
 Phe Asp Phe Tyr Asp Pro Lys Thr Pro Phe Phe Thr Ala Pro Arg Cys  
     370                         375                         380  
  
 ttg cct ccg acg caa ttg gac aag tgc aag atg aaa tat gtn ttt atc 1203  
 Leu Pro Pro Thr Gln Leu Asp Lys Cys Lys Met Lys Tyr Val Phe Ile  
     385                         390                         395  
  
 tca gat ggt tgc tta ctg aga gaa tgc aac atc gag cat tct gtg att 1251  
 Ser Asp Gly Cys Leu Leu Arg Glu Cys Asn Ile Glu His Ser Val Ile  
     400                         405                         410  
  
 gga gtc tgc tca cgt gtc agc tct gga tgt gaa ctc aag gac tcc gtg 1299  
 Gly Val Cys Ser Arg Val Ser Ser Gly Cys Glu Leu Lys Asp Ser Val  
     415                         420                         425                         430  
  
 atg atg gga gcg gac atc tat gaa act gaa gaa gct tca aag cta 1347  
 Met Met Gly Ala Asp Ile Tyr Glu Thr Glu Glu Glu Ala Ser Lys Leu  
     435                         440                         445  
  
 ctg tta gct ggg aag gtc ccr gtt gga ata gga agg aac aca aag ata 1395  
 Leu Leu Ala Gly Lys Val Pro Val Gly Ile Gly Arg Asn Thr Lys Ile  
     450                         455                         460  
  
 agg aac tgt atc att gac atg aat gct agg att ggg aag aac gtg gtg 1443  
 Arg Asn Cys Ile Ile Asp Met Asn Ala Arg Ile Gly Lys Asn Val Val  
     465                         470                         475  
  
 atc aca aac agt aag ggc atc caa gag gct gat cac ccg gaa gaa ggg 1491  
 Ile Thr Asn Ser Lys Gly Ile Gln Glu Ala Asp His Pro Glu Glu Gly  
     480                         485                         490  
  
 tac tac ata agg tct gga atc gtg gtg atc ctg aag aat gca acc atc 1539  
 Tyr Tyr Ile Arg Ser Gly Ile Val Val Ile Leu Lys Asn Ala Thr Ile  
     495                         500                         505                         510  
  
 aac gat ggg tct gtc ata tagatcggt gcgtktgcg 1576  
 Asn Asp Gly Ser Val Ile  
     515  
  
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 <211> 516  
 <212> PRT  
 <213> Zea mays  
  
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 Met Gln Phe Ala Leu Ala Leu Asp Thr Asn Ser Gly Pro His Gln Ile  
     1                         5                             10                         15  
  
 Arg Ser Cys Glu Gly Asp Gly Ile Asp Arg Leu Glu Lys Leu Ser Ile  
     20                         25                             30  
  
 Gly Gly Arg Lys Gln Glu Lys Ala Leu Arg Asn Arg Cys Phe Gly Gly  
     35                         40                             45  
  
 Arg Val Ala Ala Thr Thr Gln Cys Ile Leu Thr Ser Asp Ala Cys Pro

50

55

60

Glu	Thr	Leu	His	Ser	Gln	Thr	Gln	Ser	Ser	Arg	Lys	Asn	Tyr	Ala	Asp
65					70					75				80	
Ala	Asn	Arg	Val	Ser	Ala	Ile	Ile	Leu	Gly	Gly	Gly	Thr	Gly	Ser	Gln
			85					90				95			
Leu	Phe	Pro	Leu	Thr	Ser	Thr	Arg	Ala	Thr	Pro	Ala	Val	Pro	Val	Gly
	100					105					110				
Gly	Cys	Tyr	Arg	Leu	Ile	Asp	Ile	Pro	Met	Ser	Asn	Cys	Phe	Asn	Ser
	115					120					125				
Gly	Ile	Asn	Lys	Ile	Phe	Val	Met	Ser	Gln	Phe	Asn	Ser	Thr	Ser	Leu
	130					135				140					
Asn	Arg	His	Ile	His	Arg	Thr	Tyr	Leu	Glu	Gly	Gly	Ile	Asn	Phe	Ala
145					150				155				160		
Asp	Gly	Ser	Val	Gln	Val	Leu	Ala	Ala	Thr	Gln	Met	Pro	Glu	Glu	Pro
	165						170					175			
Val	Gly	Trp	Phe	Gln	Gly	Thr	Ala	Asp	Ser	Ile	Arg	Lys	Phe	Ile	Trp
	180						185				190				
Val	Leu	Glu	Asp	Tyr	Tyr	Ser	His	Lys	Ser	Ile	Asp	Asn	Ile	Val	Ile
	195						200				205				
Leu	Ser	Gly	Asp	Gln	Leu	Tyr	Arg	Met	Asn	Tyr	Met	Glu	Leu	Val	Gln
	210					215				220					
Lys	His	Val	Glu	Asp	Asp	Ala	Asp	Ile	Thr	Ile	Ser	Cys	Ala	Pro	Val
225					230					235				240	
Asp	Glu	Ser	Arg	Ala	Ser	Lys	Asn	Gly	Leu	Val	Lys	Ile	Asp	His	Thr
	245						250					255			
Gly	Arg	Val	Leu	Gln	Phe	Phe	Glu	Lys	Pro	Lys	Gly	Ala	Asp	Leu	Asn
	260						265				270				
Ser	Met	Arg	Val	Glu	Thr	Asn	Phe	Leu	Ser	Tyr	Ala	Ile	Asp	Asp	Ala
	275						280				285				
Gln	Lys	Tyr	Pro	Tyr	Leu	Ala	Ser	Met	Gly	Ile	Tyr	Val	Phe	Lys	Lys
	290						295				300				
Asp	Ala	Leu	Leu	Asp	Leu	Leu	Lys	Ser	Lys	Tyr	Thr	Gln	Leu	His	Asp
305					310					315				320	
Phe	Gly	Ser	Glu	Ile	Leu	Pro	Arg	Ala	Val	Leu	Asp	His	Ser	Val	Gln
	325						330					335			
Ala	Cys	Ile	Phe	Thr	Gly	Tyr	Trp	Glu	Asp	Val	Gly	Thr	Ile	Lys	Ser
	340						345					350			
Phe	Phe	Asp	Ala	Asn	Leu	Ala	Leu	Thr	Glu	Gln	Pro	Ser	Lys	Phe	Asp

355

360

365

Phe Tyr Asp Pro Lys Thr Pro Phe Phe Thr Ala Pro Arg Cys Leu Pro  
 370 375 380

Pro Thr Gln Leu Asp Lys Cys Lys Met Lys Tyr Val Phe Ile Ser Asp  
 385 390 395 400

Gly Cys Leu Leu Arg Glu Cys Asn Ile Glu His Ser Val Ile Gly Val  
 405 410 415

Cys Ser Arg Val Ser Ser Gly Cys Glu Leu Lys Asp Ser Val Met Met  
 420 425 430

Gly Ala Asp Ile Tyr Glu Thr Glu Glu Glu Ala Ser Lys Leu Leu Leu  
 435 440 445

Ala Gly Lys Val Pro Val Gly Ile Gly Arg Asn Thr Lys Ile Arg Asn  
 450 455 460

Cys Ile Ile Asp Met Asn Ala Arg Ile Gly Lys Asn Val Val Ile Thr  
 465 470 475 480

Asn Ser Lys Gly Ile Gln Glu Ala Asp His Pro Glu Glu Gly Tyr Tyr  
 485 490 495

Ile Arg Ser Gly Ile Val Val Ile Leu Lys Asn Ala Thr Ile Asn Asp  
 500 505 510

Gly Ser Val Ile  
 515

&lt;210&gt; 41

&lt;211&gt; 1576

&lt;212&gt; DNA

&lt;213&gt; Zea mays

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (10)..(1563)

<223> Shrunken-2 gene revertant form, modified to be  
heat stable

&lt;220&gt;

&lt;221&gt; variation

&lt;222&gt; (267)

&lt;223&gt; k = g or t; amino acid 86 = Ala.

&lt;220&gt;

&lt;221&gt; variation

&lt;222&gt; (540)

&lt;223&gt; n = a or g or c or t/u, unknown, or other.

&lt;220&gt;

&lt;221&gt; variation

&lt;222&gt; (1008)

<223> y = c or t.

<220>

<221> variation

<222> (1197)

<223> n = a or g or c or t/u, unknown, or other.

<220>

<221> variation

<222> (1368)

<223> r = a or g; amino acid 453 = Pro.

<220>

<221> variation

<222> (1572)

<223> k = g or t.

<400> 41

ggaggagat atg cag ttt gca ctt gca ttg gac acg aac tca ggt cct cac	51
Met Gln Phe Ala Leu Ala Leu Asp Thr Asn Ser Gly Pro His	
1	5
	10

cag ata aga tct tgt gag ggt gat ggg att gag agg ttg gaa aaa tta	99
Gln Ile Arg Ser Cys Glu Gly Asp Gly Ile Asp Arg Leu Glu Lys Leu	
15	20
	25
	30

agt att ggg ggc aga aag cag gag aaa gct ttg aga aat agg tgc ttt	147
Ser Ile Gly Gly Arg Lys Gln Glu Lys Ala Leu Arg Asn Arg Cys Phe	
35	40
	45

ggg ggt aga gtt gca act aca caa tgt att ctt acc tca gat gct	195
Gly Gly Arg Val Ala Ala Thr Thr Gln Cys Ile Leu Thr Ser Asp Ala	
50	55
	60

tgt cct gaa act ctt cat tct caa aca cag tcc tct agg aaa aat tat	243
Cys Pro Glu Thr Leu His Ser Gln Thr Gln Ser Ser Arg Lys Asn Tyr	
65	70
	75

gct gat gca aac cgt gta tct gck atc att ttg ggc gga ggc act gga	291
Ala Asp Ala Asn Arg Val Ser Ala Ile Ile Leu Gly Gly Thr Gly	
80	85
	90

tct cag ctc ttt cct ctg aca agc aca aga gct acg cct gct gta cct	339
Ser Gln Leu Phe Pro Leu Thr Ser Thr Arg Ala Thr Pro Ala Val Pro	
95	100
	105
	110

gtt gga gga tgt tac agg ctt att gat atc cct atg agt aac tgc ttc	387
Val Gly Gly Cys Tyr Arg Leu Ile Asp Ile Pro Met Ser Asn Cys Phe	
115	120
	125

aac agt ggt ata aat aag ata ttt gtg atg agt cag ttc aat tct act	435
Asn Ser Gly Ile Asn Lys Ile Phe Val Met Ser Gln Phe Asn Ser Thr	
130	135
	140

tcg ctt aac cgc cat att cat cgt aca tac ctt gaa ggc ggg atc aac	483
Ser Leu Asn Arg His Ile His Arg Thr Tyr Leu Glu Gly Gly Ile Asn	
145	150
	155

ttt gct gat gga tct gta cag gta tta gcg gct aca caa atg cct gaa Phe Ala Asp Gly Ser Val Gln Val Leu Ala Ala Thr Gln Met Pro Glu 160 165 170	531
gag cca gtn gga tgg ttc cag ggt aca gca gac tct atc aga aaa ttt Glu Pro Val Gly Trp Phe Gln Gly Thr Ala Asp Ser Ile Arg Lys Phe 175 180 185 190	579
atc tgg gta ctc gag gat tat tac agt cac aaa tcc att gac aac att Ile Trp Val Leu Glu Asp Tyr Tyr Ser His Lys Ser Ile Asp Asn Ile 195 200 205	627
gta atc ttg agt ggc gat cag ctt tat cgg atg aat tac atg gaa ctt Val Ile Leu Ser Gly Asp Gln Leu Tyr Arg Met Asn Tyr Met Glu Leu 210 215 220	675
gtg cag aaa cat gtc gag gac gat gct gat atc act ata tca tgt gct Val Gln His Val Glu Asp Asp Ala Asp Ile Thr Ile Ser Cys Ala 225 230 235	723
cct gtt gat gag agc cga gct tct aaa aat ggg cta gtg aag att gat Pro Val Asp Glu Ser Arg Ala Ser Lys Asn Gly Leu Val Lys Ile Asp 240 245 250	771
cat act gga cgt gta ctt caa ttc ttt gaa aaa cca aag ggt gct gat His Thr Gly Arg Val Leu Gln Phe Phe Glu Lys Pro Lys Gly Ala Asp 255 260 265 270	819
tgc aat tct atg aga gtt gag acc aac ttc ctg agc tat gct ata gat Leu Asn Ser Met Arg Val Glu Thr Asn Phe Leu Ser Tyr Ala Ile Asp 275 280 285	867
gat gca cag aaa tat cca tac ctt gca tca atg ggc att tat gtc ttc Asp Ala Gln Lys Tyr Pro Tyr Leu Ala Ser Met Gly Ile Tyr Val Phe 290 295 300	915
aag aaa gat gca ctt tta gac ctt ctc aag tca aaa tat act caa tta Lys Lys Asp Ala Leu Leu Asp Leu Leu Lys Ser Lys Tyr Thr Gln Leu 305 310 315	963
cat gac ttt gga tct gaa atc ctc cca aga gct gta cta gat tay agt His Asp Phe Gly Ser Glu Ile Leu Pro Arg Ala Val Leu Asp Tyr Ser 320 325 330	1011
gtg cag gca tgc att ttt acg ggc tat tgg gag gat gtt gga aca atc Val Gln Ala Cys Ile Phe Thr Gly Tyr Trp Glu Asp Val Gly Thr Ile 335 340 345 350	1059
aaa tca ttc ttt gat gca aac ttg gcc ctc act gag cag cct tcc aag Lys Ser Phe Asp Ala Asn Leu Ala Leu Thr Glu Gln Pro Ser Lys 355 360 365	1107
ttt gat ttt tac gat cca aaa aca cct ttc act gca ccc cga tgc Phe Asp Phe Tyr Asp Pro Lys Thr Pro Phe Phe Thr Ala Pro Arg Cys 370 375 380	1155

ttg cct ccg acg caa ttg gac aag tgc aag atg aaa tat gtn ttt atc Leu Pro Pro Thr Gln Leu Asp Lys Cys Lys Met Lys Tyr Val Phe Ile 385 390 395	1203
tca gat ggt tgc tta ctg aga gaa tgc aac atc gag cat tct gtg att Ser Asp Gly Cys Leu Leu Arg Glu Cys Asn Ile Glu His Ser Val Ile 400 405 410	1251
gga gtc tgc tca cgt gtc agc tct gga tgt gaa ctc aag gac tcc gtg Gly Val Cys Ser Arg Val Ser Ser Gly Cys Glu Leu Lys Asp Ser Val 415 420 425 430	1299
atg atg gga gcg gac atc tat gaa act gaa gaa gaa gct tca aag cta Met Met Gly Ala Asp Ile Tyr Glu Thr Glu Glu Ala Ser Lys Leu 435 440 445	1347
ctg tta gct ggg aag gtc ccr gtt gga ata gga agg aac aca aag ata Leu Leu Ala Gly Lys Val Pro Val Gly Ile Gly Arg Asn Thr Lys Ile 450 455 460	1395
agg aac tgt atc att gac atg aat gct agg att ggg aag aac gtg gtg Arg Asn Cys Ile Ile Asp Met Asn Ala Arg Ile Gly Lys Asn Val Val 465 470 475	1443
atc aca aac agt aag ggc atc caa gag gct gat cac ccg gaa gaa ggg Ile Thr Asn Ser Lys Gly Ile Gln Glu Ala Asp His Pro Glu Glu Gly 480 485 490	1491
tac tac ata agg tct gga atc gtg gtg atc ctg aag aat gca acc atc Tyr Tyr Ile Arg Ser Gly Ile Val Val Ile Leu Lys Asn Ala Thr Ile 495 500 505 510	1539
aac gat ggg tct gtc ata tagatcggt gcgtktgcg Asn Asp Gly Ser Val Ile 515	1576

<210> 42  
<211> 516  
<212> PRT  
<213> Zea mays

<400> 42

Met Gln Phe Ala Leu Ala Leu Asp Thr Asn Ser Gly Pro His Gln Ile 1 5 10 15
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Arg Ser Cys Glu Gly Asp Gly Ile Asp Arg Leu Glu Lys Leu Ser Ile 20 25 30
---

Gly Gly Arg Lys Gln Glu Lys Ala Leu Arg Asn Arg Cys Phe Gly Gly 35 40 45
---

Arg Val Ala Ala Thr Thr Gln Cys Ile Leu Thr Ser Asp Ala Cys Pro 50 55 60
---

Glu Thr Leu His Ser Gln Thr Gln Ser Ser Arg Lys Asn Tyr Ala Asp

65	70	75	80
Ala Asn Arg Val Ser Ala Ile Ile Leu Gly	Gly Gly Thr Gly Ser Gln		
85	90	95	
Leu Phe Pro Leu Thr Ser Thr Arg Ala Thr	Pro Ala Val Pro Val Gly		
100	105	110	
Gly Cys Tyr Arg Leu Ile Asp Ile Pro Met	Ser Asn Cys Phe Asn Ser		
115	120	125	
Gly Ile Asn Lys Ile Phe Val Met Ser Gln	Phe Asn Ser Thr Ser Leu		
130	135	140	
Asn Arg His Ile His Arg Thr Tyr Leu Glu	Gly Gly Ile Asn Phe Ala		
145	150	155	160
Asp Gly Ser Val Gln Val Leu Ala Ala Thr	Gln Met Pro Glu Glu Pro		
165	170	175	
Val Gly Trp Phe Gln Gly Thr Ala Asp Ser	Ile Arg Lys Phe Ile Trp		
180	185	190	
Val Leu Glu Asp Tyr Tyr Ser His Lys Ser	Ile Asp Asn Ile Val Ile		
195	200	205	
Leu Ser Gly Asp Gln Leu Tyr Arg Met Asn	Tyr Met Glu Leu Val Gln		
210	215	220	
Lys His Val Glu Asp Asp Ala Asp Ile Thr	Ile Ser Cys Ala Pro Val		
225	230	235	240
Asp Glu Ser Arg Ala Ser Lys Asn Gly	Leu Val Lys Ile Asp His Thr		
245	250	255	
Gly Arg Val Leu Gln Phe Phe Glu	Lys Pro Lys Gly Ala Asp Leu Asn		
260	265	270	
Ser Met Arg Val Glu Thr Asn Phe Leu Ser	Tyr Ala Ile Asp Asp Ala		
275	280	285	
Gln Lys Tyr Pro Tyr Leu Ala Ser Met Gly	Ile Tyr Val Phe Lys Lys		
290	295	300	
Asp Ala Leu Leu Asp Leu Leu Lys Ser Lys	Tyr Thr Gln Leu His Asp		
305	310	315	320
Phe Gly Ser Glu Ile Leu Pro Arg Ala Val	Leu Asp Tyr Ser Val Gln		
325	330	335	
Ala Cys Ile Phe Thr Gly Tyr Trp	Glu Asp Val Gly Thr Ile Lys Ser		
340	345	350	
Phe Phe Asp Ala Asn Leu Ala Leu Thr	Glu Gln Pro Ser Lys Phe Asp		
355	360	365	
Phe Tyr Asp Pro Lys Thr Pro Phe Phe Thr	Ala Pro Arg Cys Leu Pro		

370

375

380

Pro Thr Gln Leu Asp Lys Cys Lys Met Lys Tyr Val Phe Ile Ser Asp  
385 390 395 400

Gly Cys Leu Leu Arg Glu Cys Asn Ile Glu His Ser Val Ile Gly Val  
405 410 415

Cys Ser Arg Val Ser Ser Gly Cys Glu Leu Lys Asp Ser Val Met Met  
420 425 430

Gly Ala Asp Ile Tyr Glu Thr Glu Glu Glu Ala Ser Lys Leu Leu Leu  
435 440 445

Ala Gly Lys Val Pro Val Gly Ile Gly Arg Asn Thr Lys Ile Arg Asn  
450 455 460

Cys Ile Ile Asp Met Asn Ala Arg Ile Gly Lys Asn Val Val Ile Thr  
465 470 475 480

Asn Ser Lys Gly Ile Gln Glu Ala Asp His Pro Glu Glu Gly Tyr Tyr  
485 490 495

Ile Arg Ser Gly Ile Val Val Ile Leu Lys Asn Ala Thr Ile Asn Asp  
500 505 510

Gly Ser Val Ile  
515